

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 6, 2004, 11:37:30 ; Search time 41 Seconds
(without alignments)
50.328 Million cell updates/sec

Title: US-09-618-577-28
Perfect score: 68
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /Geneseq_19Jun03:.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	AA28333	Antigenic syntheti
2	68	100.0	147	AAW17911	Peptide CFA/I from
3	68	100.0	170	AAW38341	E. coli colonisati
4	54	79.4	10	AA28324	Antigenic syntheti
5	54	79.4	10	AA28334	Antigenic syntheti
6	47	69.1	167	AAW50340	ERIC CS4 pilus Csa
7	41	60.3	537	AAW41863	Arabidopsis thalia
8	41	60.3	569	AAW41862	Arabidopsis thalia
9	41	60.3	577	AAW41861	Arabidopsis thalia

10	41	60.3	1379	22	ABB68940	Drosophila melanog
11	40	58.8	57	22	AAU65565	Propionibacterium
12	40	58.8	263	22	AAU39542	Propionibacterium
13	40	58.8	348	21	AA20258	Arabidopsis thalia
14	40	58.8	362	21	AA20257	Arabidopsis thalia
15	40	58.8	362	22	AAE02530	Arabidopsis thalia
16	40	58.8	374	21	AA20256	Arabidopsis thalia
17	40	58.8	665	21	AA20255	Arabidopsis thalia
18	40	58.8	745	21	AA20254	Arabidopsis thalia
19	40	58.8	951	21	AA20253	Arabidopsis thalia
20	39	57.4	60	22	AAU56836	Propionibacterium
21	39	57.4	60	22	AAU62420	Propionibacterium
22	39	57.4	333	14	AA31019	Grass pollen aller
23	39	57.4	333	20	AA25681	Grass pollen aller
24	39	57.4	376	19	AAW81744	M. tuberculosis im
25	39	57.4	376	19	AAW64377	Mycobacterium tube
26	39	57.4	376	20	AA39174	M. tuberculosis an
27	39	57.4	376	20	AA39031	M. tuberculosis re
28	39	57.4	1291	19	AAW59912	Amino acid sequenc
29	38	55.9	152	24	ABR01187	Human gene 241-enc
30	38	55.9	153	21	AAW40180	Human secreted pro
31	38	55.9	295	22	AAW70141	Ebola virus glycop
32	38	55.9	363	22	AAU01253	B. subtilis live h
33	38	55.9	556	22	AAW51854	Human protein sequ
34	38	55.9	676	21	AAW70074	Ebola virus glycop
35	38	55.9	676	21	AAW77112	Ebola virus glycop
36	38	55.9	676	22	AAE00706	Ebola virus strain
37	38	55.9	676	22	AAW70133	Ebola virus glycop
38	38	55.9	676	24	ABJ18477	Chimeric filovirus
39	38	55.9	733	21	ABW41232	Human ORF996
40	38	55.9	747	24	ABJ18472	Chimeric filovirus
41	38	55.9	1744	22	ABW62890	Drosophila melanog
42	37	54.4	125	24	ABU00090	Human novel polype
43	37	54.4	140	22	AA003622	Human polypeptide
44	37	54.4	344	18	AAW32425	Mycobacterium tube
45	37	54.4	344	18	AAW32357	Mycobacterium tube

ALIGNMENTS

RESULT 1
AA28333
ID AAR28333 standard; peptide; 13 AA.
AC AAR28333;
XX 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX Antigenic synthetic peptide contg. B-cell epitope 124.
XX CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.
XX Synthetic.
XX W09219263-A1.
XX 12-NOV-1992
XX 13-MAY-1991; 91WO-US03328.
XX 24-APR-1991; 91US-0690485.
XX (USSA) US SEC OF ARMY.
XX Boedeker EC, Cassels FU, Jarboe D, Reid RH, Setterstrom JA;
XX WPI; 1992-398530/48.
XX Protection against entero-pathogenic organisms - comprises oral
XX admn. of compsn. consisting of synthetic peptide contg. CFA-I
XX pilus protein T-cell epitope(s) and/or B-cell epitope(s)

PT encapsulated in biodegradable polymeric matrix
 XX
 PS Claim 36; Page 76; 121pp; English.
 XX
 CC The sequence is that of an antigenic synthetic peptide contg. CFA/I
 CC plus protein B-cell epitopes which may be encapsulated within a
 CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-
 CC glycolide) having a relative ratio between the amt. of lactide and
 CC glycolide components within the range of 48:52 to 52:48 for use as a
 CC vaccine for the immunisation of a human or other mammal against
 CC infection by enteropathogenic organisms. This provides extremely
 CC effective protection against bacterial or viral infections in the
 CC tissue of a mammal. It protects against bacteria including *Salmonella*
 CC typhi, *Shigella sonnei*, *S. flexneri*, *S. dysenteriae*, *S. boydii*,
 CC *E. coli*, *Vibrio cholerae*, *Yersinia*, *Staphylococcus*, *Clostridium* and
 CC campylobacter. Viruses protected against include hepatitis A,
 CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,
 CC varicella-zoster virus, Epstein-Barr virus and cytomegaloviruses
 CC See also AAR28315-R28334.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 13 AA;
 QY Query Match 100.0%; Score 68; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 KTAGTAPTAGNYS 13
 QY 1 KTAGTAPTAGNYS 13
 DB 1 KTAGTAPTAGNYS 13

RESULT 2
 AAM17911
 ID AAM17911 standard; peptide; 147 AA.
 XX
 AC AAM17911;
 XX
 DT 25-JUL-1997 (first entry)
 XX
 DE Peptide CFA/I from denatured protein subunits of *E. coli* fimbriae.
 XX
 KW Immunisation; fimbrial protein; colonisation factor antigen;
 XX antibody.
 XX
 OS *Escherichia coli*.
 OS Synthetic.
 XX
 PN WO9638171-A1.
 XX
 PD 05-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US08730.
 XX
 PR 02-JUN-1995; 95US-0460617.
 XX
 PA (USSA) US DEPT OF THE ARMY.
 XX
 PI Anderson J, Carter JM, Casseels F;
 XX
 DR WPI; 1997-034101/03.
 XX
 PT New consensus peptide from fimbrial proteins of the *E. coli* family
 PT CS4-CFA/I - and denatured fimbrial proteins, used for immunisation
 PT against infection by bacteria of this family
 XX
 PS Disclosure; Page 4; 17pp; English.
 XX
 CC The present sequence is a peptide from the denatured protein subunit
 CC of fimbriae from CFA/I. Many of the denatured proteins give rise to
 CC antibodies that are reactive with proteins of other strains as shown
 CC by precipitation studies on nitrocellulose. They are also reactive
 CC with surface antigens of the fimbriae as shown by agglutination

CC of organisms. They can be used to immunise against disease caused by
 CC enterotoxigenic *E. coli* of the family CS4-CFA/I. Also antibodies raised
 CC against the *E. coli* CS4-CFA/I family can be used as diagnostic reagents
 CC to identify antigens.
 XX
 SQ Sequence 147 AA;
 QY Query Match 100.0%; Score 68; DB 18; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 124 KTAGTAPTAGNYS 136
 QY 1 KTAGTAPTAGNYS 13
 DB 124 KTAGTAPTAGNYS 136

RESULT 3
 AAM38341
 ID AAM38341 standard; Protein; 170 AA.
 XX
 AC AAM38341;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE *E. coli* colonisation factor antigen CFAI.
 XX
 KW Bacterial colonisation; colonisation factor antigen; CFAI;
 KW enterotoxigenic *Escherichia coli*; vaccine; diagnosis; research.
 XX
 OS *Escherichia coli*.
 XX
 PN US5698416-A.
 XX
 PD 16-DEC-1997.
 XX
 PF 02-JUN-1995; 95US-0460739.
 XX
 PR 02-JUN-1995; 95US-0460739.
 XX
 PA (USSA) US SEC OF ARMY.
 XX
 PI Bell BA, Casseels FJ, Wolf MK;
 XX
 DR WPI; 1998-051486/05.
 DR N-PSDB; AAT96059.
 XX
 PT Production of bacterial colonisation factor protein - by expression
 PT under control of heat-inducible promoter
 XX
 PS Example 2; Columns 15-18; 11pp; English.
 XX
 CC Production of a protein that affects bacterial colonisation,
 CC comprises inoculating a broth containing tryptone and yeast extract
 CC with enteric bacteria containing a DNA sequence encoding the
 CC protein under the control of a temperature regulated promoter,
 CC culturing the bacteria, removing the bacteria from the medium and
 CC recovering the protein. The method is used especially for producing
 CC the colonisation factor antigen CFAI of enterotoxigenic *E. coli*, i.e.
 CC the antigen denoted by the present sequence, which may be used in
 CC vaccines or for diagnostic or research purposes. Growing the
 CC bacteria at low temperature until the late logarithmic phase
 CC increases the yield of the protein.
 CC
 SQ Sequence 170 AA;
 QY Query Match 100.0%; Score 68; DB 19; Length 170;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 147 KTAGTAPTAGNYS 159
 QY 1 KTAGTAPTAGNYS 13
 DB 147 KTAGTAPTAGNYS 159

```

RESULT 4
DE AAR28324 standard; peptide; 10 AA.
XX
AC AAR28324;
XX
DT 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX
DE Antigenic synthetic peptide contg. T-cell epitope 126.
XX
KW CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.
XX
OS Synthetic.
XX
PN WO9219263-A1.
XX
PD 12-NOV-1992.
XX
PF 13-MAY-1991; 91WO-US03328.
XX
PR 24-APR-1991; 91US-0690485.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Boedeker EC, Cassels FJ, Jarboe D, Reid RH, Setterstrom JA;
XX
WPI; 1992-398530/48.
XX
PT Protection against entero-pathogenic organisms - comprises oral
PT admin. of compsn. consisting of synthetic peptide contg. CFA-I
PT pilus protein T-cell epitope(s) and/or B-cell epitope(s)
PT encapsulated in biodegradable polymeric matrix
XX
XX
PS Claim 23; Page 76; 121pp; English.
XX
CC The sequence is that of an antigenic synthetic peptide contg. CFA/I
CC plus protein T-cell epitopes which may be encapsulated within a
CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-
CC glycolide) having a relative ratio between the amt. of lactide and
CC glycolide components within the range of 48:52 to 52:48 for use as a
CC vaccine for the immunisation of a human or other mammal against
CC infection by enteropathogenic organisms. This provides extremely
CC effective protection against bacterial or viral infections in the
CC tissue of a mammal. It protects against bacteria including Salmonella
CC typhi, Shigella sonnei, S. flexneri, S. dysenteriae, S. boydii,
CC E.coli, Vibrio cholera, Yersinia, staphylococcus, clostridium and
CC campylobacter. Viruses protected against include hepatitis A,
CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,
CC Varicella-Zoster virus, Epstein-Barr virus and cytomegaloviruses
CC See also AAR28315-R28334.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
XX
Query Match 79.4%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGTAPTAGNY 12
DB 1 AGTAPTAGNY 10
XX
RESULT 5
DE AAR28334 standard; peptide; 10 AA.
XX
AC AAR28334;
XX
DT 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX

```

```

XX
XX Antigenic synthetic peptide contg. B-cell epitope 127.
XX
KW CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.
XX
OS Synthetic.
XX
PN WO9219263-A1.
XX
PD 12-NOV-1992.
XX
PF 13-MAY-1991; 91WO-US03328.
XX
PR 24-APR-1991; 91US-0690485.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Boedeker EC, Cassels FJ, Jarboe D, Reid RH, Setterstrom JA;
XX
WPI; 1992-398530/48.
XX
PT Protection against entero-pathogenic organisms - comprises oral
PT admin. of compsn. consisting of synthetic peptide contg. CFA-I
PT pilus protein T-cell epitope(s) and/or B-cell epitope(s)
PT encapsulated in biodegradable polymeric matrix
XX
XX
PS Claim 35; Page 76; 121pp; English.
XX
CC The sequence is that of an antigenic synthetic peptide contg. CFA/I
CC plus protein B-cell epitopes which may be encapsulated within a
CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-
CC glycolide) having a relative ratio between the amt. of lactide and
CC glycolide components within the range of 48:52 to 52:48 for use as a
CC vaccine for the immunisation of a human or other mammal against
CC infection by enteropathogenic organisms. This provides extremely
CC effective protection against bacterial or viral infections in the
CC tissue of a mammal. It protects against bacteria including Salmonella
CC typhi, Shigella sonnei, S. flexneri, S. dysenteriae, S. boydii,
CC E.coli, Vibrio cholera, Yersinia, staphylococcus, clostridium and
CC campylobacter. Viruses protected against include hepatitis A,
CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,
CC Varicella-Zoster virus, Epstein-Barr virus and cytomegaloviruses.
CC See also AAR28315-R28333.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
XX
Query Match 79.4%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTAPTAGNYS 13
DB 1 GTAPTAGNYS 10
XX
RESULT 6
DE AAM50340 standard; Protein; 167 AA.
XX
AC AAM50340;
XX
DT 18-FEB-2002 (first entry)
XX
DE ETEC CS4 pilus CsaB fimbrial structural protein.
XX
KW CS4 pilus; enterotoxigenic; ETEC; csa operon; CsaB; fimbrial;
KW vaccine; diarrhoea; antibacterial; antidiarrhetic.
XX
OS Escherichia coli.
XX
XX
XX Key Location/Qualifiers
XX
FT Peptide 1..23
XX

```

FT Protein /label= Signal_peptide
FT 24..167
FT /label= Mature_protein
XX MO200181582-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US12914.
XX
XX 20-APR-2000; 2000US-198686P.
XX
XX (UTMA-) UNIV MARYLAND BALTIMORE.
XX
XX Altdoun Z, Levine NM, Barry EM;
XX
XX MPI: 2002-049280/06.
XX N-PSDB; AAI70760, AAI70780.
XX
XX New nucleotide sequence, useful as immunogenic agent for generating
PT immune response against recombinant product of the operon, comprises
PT csa operon which encodes enterotoxigenic Escherichia coli-CS4 pili
XX
XX Claim 4; Page 50; 81pp; English.
XX
XX The present sequence is that of fimbrial structural protein CsaB
CC of enterotoxigenic Escherichia coli (ETEC) strain E11881A. CsaB is
CC encoded by the csaB gene (see AAI70760) of the E. coli E11881A csa
CC operon. This operon has 5 contiguous genes, csaA-csaE, which encode
CC the synthesis of ETEC-CS4 pili. It has been expressed in attenuated
CC Shigella strain CVD1204 guaha, constructing the Shigella expressing
CC CS4 fimbriae vaccine strain CVD1204 (pGA2-CS4). The CsaB protein
CC has a calculated mol. wt. of 17343.9 and a theoretical pI of 6.56.
CC It shares homology with other ETEC fimbriae proteins. Recombinant
CC CsaA-CsaE polypeptides are used in claimed immunogenic compositions
CC to generate an immune response in a subject. These prevent ETEC
CC colonisation, and hence protect against diarrhoea.
XX
XX Sequence 167 AA:
SQ
Query Match 69.1%; Score 47; DB 23; Length 167;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TAGTAPTAGNYS 13
DB 145 TTAQAPTAGNYS 156
RESULT 7
AAG41863
ID AAG41863 standard; Protein; 537 AA.
XX
XX AAG41863;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 52138.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
XX
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX
XX 05-MAR-1999; 99US-0123180.
PR

PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143544.
PR 14-JUL-1999; 99US-0143624.

```

PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147302.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155133.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157111.
PR 05-OCT-1999; 99US-0157753.

```

```

PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 60.3%; Score 41; DB 21; Length 537;
Best Local Similarity 61.5%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Cy 1 KTAGTAPTAGNYS 13
Db 499 RTGCTAPBGRNYS 511

```

```

RESULT 8
AAG41862
ID AAG41862 standard; Protein; 569 AA.
XX AC AAG41862;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52137.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 23-MAR-1999; 99US-0123548.
PR 25-MAR-1999; 99US-0125788.
PR 29-MAR-1999; 99US-0126254.
PR 01-APR-1999; 99US-0126785.
PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 99US-0128714.

```

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143442.
PR 14-JUL-1999; 99US-0143524.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154179.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.

PR 14-OCT-1999; 99US-0159328.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 41; DB 21; Length 569;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTAGTAPAGNYS 13
: |||||
Db 531 RTGTAPEGFNYS 543

RESULT 9

AA641861
ID AA641861 standard; Protein; 577 AA.

XX AA641861;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52136.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX KW Arabidopsis thaliana.

XX OS Arabidopsis thaliana.

XX PN EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX XX 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123546.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 28-APR-1999; 99US-0130891.

XX PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132853.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 03-AUG-1999; 99US-0146389.
 PR 04-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149829.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151086.
 PR 30-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.

PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 26-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161923.
 PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 41; DB 21; Length 577;
 Best Local Similarity 61.5%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTACTAPTRAGNYS 13
 Db 539 RTGTAPGPFNYS 551

RESULT 10

ABR68940
 ID ABR68940 standard; Protein, 1379 AA.

XX ABR68940;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 33612.

XX Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL13043.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell
 interactions -

XX Dislosure; SEQ ID NO 33612; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins
 (ABR57737-ABR72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1379 AA;

Query Match 60.3%; Score 41; DB 22; Length 1379;
Best Local Similarity 63.6%; Pred. No. 3.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAGN 12
Db 1049 SAGTSPTASSY 1059

RESULT 11

AAU65565
ID AAU65565 standard; Protein; 57 AA.

XX AAU65565;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #26461.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JU, Wang SS, Bhatia A;
PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59676.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -

XX Example 1; SEQ ID No 26760; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 57 AA;

Query Match 58.8%; Score 40; DB 22; Length 57;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAG 10
Db 19 TASTAPTAG 27

RESULT 12

AAU39542
ID AAU39542 standard; Protein; 263 AA.

XX AAU39542;

XX 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #438.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JU, Wang SS, Bhatia A;
PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59507.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -

XX Example 1; SEQ ID No 737; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.

SO Sequence 263 AA;

Query Match 58.8%; Score 40; DB 22; Length 263;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 3 ACTAPTAGNYS 13
|||:|:|:|:
Db 174 AGTSPTAAQYA 184

RESULT 13

ID AGG20258 standard; Protein; 348 AA.

XX AGG20258;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 22375.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridization assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134368.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144326.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 03-AUG-1999; 99US-0146389.

PR 04-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 15-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 16-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160778.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.8%; Score 40; DB 21; Length 348;

Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KTAGTAPTACN 11
Db 290 KTAGPAPTYGH 300

RESULT 14

AGG20257 ID AGG20257 standard; Protein; 362 AA.

XX AAG20257;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 22374.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136382.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148568.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154029.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157111.
PR 05-OCT-1999; 99US-0157553.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160776.
PR 21-OCT-1999; 99US-0160777.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.8%; Score 40; DB 21; Length 362;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTAGTAPTGN 11
DB 304 KTAGPAPTYGH 314

RESULT 15
AAE02530
ID AAE02530 standard; Protein; 362 AA.
XX
XX AAE02530;
XX
XX 10-AUG-2001 (first entry)
XX
XX Arabidopsis thaliana G996 transcription factor homologue, G1349.
XX
XX Transcription factor; pesticidal; antimicrobial; gene therapy;
XX pachogen tolerance; trichome structure; callose induction;
XX phytoalexin induction; plant structure; plant development.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX Region 13..63
XX /note= "Conserved domain"
XX
XX W0200135726-A1.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000MO-US31418.
XX
XX 17-NOV-1999; 99US-0166228.
XX 17-APR-2000; 2000US-0197899.
XX 22-AUG-2000; 2000US-0227439.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX (HEAR/) HEARD J.
XX (RATC/) RATCLIFFE O.
XX (CREE/) CREELMAN R.
XX (JTAN/) JIANG C.
XX (PINE/) PINEDA O.
XX (REUB/) REUBER L.
XX (ADAM/) ADAM L.
XX
XX Heard J, Ratcliffe O, Creelman R, Jiang C, Pineda O, Reuber L,
XX Adam L;
XX
XX WPI; 2001-335978/35.
XX N-PSDB; AAD06499.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
XX for altering the pathogen resistance characteristics of plants, e.g.
XX corn, potato and cotton plants -
XX
XX
XX Claim 4; Page 129-131; 134pp; English.
XX
XX The present sequence is Arabidopsis thaliana
XX transcription factor homologue. The transcription factors are used
XX to alter the structure and developmental characteristics of plants
XX such as soybean, wheat, corn, potato, cotton, rice, oilseed rape,
XX sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry,
XX strawberry, raspberry, carrot, cantaloupe, cauliflower, cucumber,
XX coffee, eggplant, grapes, mango, lettuce, honeydew, melon, onion,
XX papaya, peppers, pineapple, spinach, squash, sweet corn, tobacco,
XX tomato, peas, watermelon, rosaceous fruits and vegetable brassicas.
XX The transcription factors are specifically useful for modifying
XX traits associated with plant's pathogen tolerance such as
XX alterations in cell wall composition, trichome number or structure,
XX callose induction, phytoalexin induction, and alterations in the
XX cell death response. Transgenic plants expressing these
XX transcription factors are more tolerant to biotrophic or necrotrophic
XX pathogens such as fungi, bacteria, molluscs, viruses, nematodes
XX and parasitic higher plants. The transcription factors are also
XX used in gene therapy.
XX
XX Sequence 362 AA;
XX

Query Match 58.8%; Score 40; DB 22; Length 362;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 1 KTAGTAPTAGN 11
||| ||| |
DB 304 KTAGPAPPTYGH 314

Search completed: February 6, 2004, 11:38:26
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:31 ; Search time 21 Seconds
(Without alignments)
26.192 Million cell updates/sec

Title: US-09-618-577-28
Perfect score: 68
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	147	5 PCT-US96-08730-9	Sequence 9, Appli
2	68	100.0	170	1 US-08-460-739-3	Sequence 3, Appli
3	68	100.0	170	2 US-08-483-101-11	Sequence 11, Appli
4	39	57.4	175	4 US-09-252-991A-30331	Sequence 30331, A
5	39	57.4	376	4 US-09-056-556-202	Sequence 202, App
6	39	57.4	376	4 US-09-072-586-197	Sequence 197, App
7	38	55.9	328	4 US-09-252-991A-26586	Sequence 26586, A
8	38	55.9	363	4 US-09-173-300-20	Sequence 20, Appli
9	38	55.9	501	4 US-09-252-991A-32936	Sequence 32936, A
10	38	55.9	676	4 US-08-760-615-2	Sequence 2, Appli
11	37	54.4	311	4 US-09-252-991A-30797	Sequence 30797, A
12	37	54.4	344	3 US-08-818-112-69	Sequence 69, Appli
13	37	54.4	344	4 US-08-818-112-70	Sequence 70, Appli
14	37	54.4	344	4 US-09-056-556-69	Sequence 69, Appli
15	37	54.4	344	4 US-09-072-596-70	Sequence 70, Appli
16	36	52.9	203	4 US-09-252-991A-22678	Sequence 22678, A
17	36	52.9	230	4 US-09-252-991A-28838	Sequence 28838, A
18	36	52.9	239	4 US-09-372-422A-42	Sequence 42, Appli
19	36	52.9	275	4 US-09-314-701-28	Sequence 28, Appli
20	36	52.9	508	4 US-09-252-991A-17386	Sequence 17386, A
21	36	52.9	680	1 US-08-542-363-4	Sequence 4, Appli
22	36	52.9	680	1 US-09-100-089-4	Sequence 4, Appli
23	36	52.9	680	4 US-09-670-827-4	Sequence 4, Appli
24	36	52.9	1620	1 US-08-542-363-2	Sequence 2, Appli
25	36	52.9	1620	3 US-09-100-089-2	Sequence 2, Appli
26	36	52.9	1620	4 US-09-670-827-2	Sequence 2, Appli
27	35.5	52.2	513	3 US-09-097-889-15	Sequence 15, Appli

28	35.5	52.2	513	4 US-09-098-079-15	Sequence 15, Appli
29	35	51.5	188	4 US-09-252-991A-24789	Sequence 24789, A
30	35	51.5	245	4 US-09-325-932A-89	Sequence 89, Appli
31	35	51.5	389	4 US-09-513-057C-23	Sequence 23, Appli
32	35	51.5	411	4 US-09-252-991A-28696	Sequence 28696, A
33	35	51.5	427	4 US-09-252-991A-17391	Sequence 17391, A
34	35	51.5	451	3 US-09-412-102-8	Sequence 8, Appli
35	35	51.5	451	3 US-09-217-787-8	Sequence 8, Appli
36	35	51.5	455	3 US-09-412-102-6	Sequence 6, Appli
37	35	51.5	455	3 US-09-412-102-10	Sequence 10, Appli
38	35	51.5	455	3 US-09-217-787-6	Sequence 6, Appli
39	35	51.5	455	3 US-09-217-787-10	Sequence 10, Appli
40	35	51.5	532	4 US-09-252-991A-30492	Sequence 30492, A
41	35	51.5	1132	4 US-09-198-452A-466	Sequence 466, App
42	35	51.5	1179	4 US-09-252-991A-17895	Sequence 17895, A
43	34	50.0	34	2 US-08-640-847C-16	Sequence 16, Appli
44	34	50.0	36	3 US-09-100-600A-10	Sequence 4, Appli
45	34	50.0	36	3 US-09-100-600A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
PCT-US96-08730-9
Sequence 9, Application PC/TUS9608730
GENERAL INFORMATION:
APPLICANT: Casseels, Frederick
APPLICANT: Anderson, Jeffrey
APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising Antibodies Against E.
TITLE OF INVENTION: Coli of the Family CSF-CFA/1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glenna Hendicks
STREET: P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: USA
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08730
FILING DATE: 03-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: PCT/US96/08730
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PCT-US96-08730-9
Query Match 100.0%; Score 68; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTAGTAPTAGNYS 13

Db 124 KTAGTAPTAGNYS 136

RESULT 2

US-08-460-739-3
; Sequence 3, Application US/08460739
; Patent No. 5698416
; GENERAL INFORMATION:
; APPLICANT: Wolf, Marcia K.
; APPLICANT: Cassels, Frederick J.
; APPLICANT: Bell, Brian A.
; TITLE OF INVENTION: Improved Methods for Production of
; TITLE OF INVENTION: Antigens Under Control of Temperature-Regulated Promoters
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glenna Hendricks
; STREET: 9669 A Main Street
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,739
; FILING DATE: 20-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna M.
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: wolf2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: CFAl protein
; US-08-460-739-3

Query Match 100.0%; Score 68; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTAGTAPTAGNYS 13
Db 147 KTAGTAPTAGNYS 159

RESULT 3

US-08-483-101-11
; Sequence 11, Application US/08483101
; Patent No. 5932715
; GENERAL INFORMATION:
; APPLICANT: Scott, June R.
; APPLICANT: Froehlich, Barbara
; APPLICANT: Caron, Judy
; TITLE OF INVENTION: CS2 Proteins and Coding Sequences
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,101
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33878
REFERENCE/DOCKET NUMBER: 6-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-483-101-11

Query Match 100.0%; Score 68; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTAGTAPTAGNYS 13
Db 147 KTAGTAPTAGNYS 159

RESULT 4

US-09-252-991A-30331
; Sequence 30331, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30331
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30331

Query Match 57.4%; Score 39; DB 4; Length 175;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KTAGTAPTAGNYS 13
Db 111 RTAGTPTARSS 123

RESULT 5

US-09-056-556-202
; Sequence 202, Application US/09056556

Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4800
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-056-556-202

Query Match 57.4%; Score 39; DB 4; Length 376;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13
Db 51 AATTPTAGYT 61

RESULT 6
US-09-072-596-197
Sequence 197, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Nevo, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Veditz, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-072-596-197

Query Match 57.4%; Score 39; DB 4; Length 376;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13
Db 51 AATTPTAGYT 61

RESULT 7
US-09-252-991A-26586
Sequence 26586, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26586
LENGTH: 328
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26586

Query Match 55.9%; Score 38; DB 4; Length 328;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13
Db 80 ASSAPVAGSY 90

RESULT 8
US-09-173-300-20
Sequence 20, Application US/09173300
Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126

;; CURRENT APPLICATION NUMBER: US/09/173,300
;; CURRENT FILING DATE: 1998-10-15
;; EARLIER APPLICATION NUMBER: 60/063,423
;; EARLIER FILING DATE: 1997 October 28
;; NUMBER OF SEQ ID NOS: 54
;; SOFTWARE: Microsoft Word Version 7.0A
;; SEQ ID NO 20
;; LENGTH: 363
;; TYPE: PRT
;; ORGANISM: Bacillus subtilis
US-09-173-300-20

Query Match 55.9%; Score 38; DB 4; Length 363;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTAPTAGNYS 13
DB 194 GNAKTAGNYA 203

RESULT 9
US-09-252-991A-32936
; Sequence 32936, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32936
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32936

Query Match 55.9%; Score 38; DB 4; Length 501;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAG 10
DB 227 TAGSCTAG 235

RESULT 10
US-08-760-615-2
; Sequence 2, Application US/08760615
; Patent No. 6200959
; GENERAL INFORMATION:
; APPLICANT: Haynes, Joel R
; APPLICANT: Schmaljohn, Connie S
; APPLICANT: Fuller, Deborah L
; APPLICANT: Schmaljohn, Alan
; APPLICANT: Jahrling, Peter B
; TITLE OF INVENTION: GENETIC INDUCTION OF ANTI-VIRAL IMMUNE
; TITLE OF INVENTION: RESPONSE AND GENETIC VACCINE FOR FILOVIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/760,615
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Berson, Bennett J
;; REGISTRATION NUMBER: 37094
;; REFERENCE/DOCKET NUMBER: 110229.91241
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 608-251-5000
;; TELEFAX: 608-251-9166
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 676 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-760-615-2

Query Match 55.9%; Score 38; DB 3; Length 676;
Best Local Similarity 46.2%; Pred. No. 1,2e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYAGTAPTAGNYS 13
DB 140 KVSCTGCPAGDPA 152

RESULT 11
US-09-252-991A-30797
; Sequence 30797, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30797
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30797

Query Match 54.4%; Score 37; DB 4; Length 311;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTAPTAGNY 12
DB 293 GSLPSAGNY 301

RESULT 12
US-08-818-112-69
; Sequence 69, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond

APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-69

Query Match 54.4%; Score 37; DB 3; Length 344;
Best Local Similarity 77.8%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11
DB 106 AGTAPTAGD 114

RESULT 13
US-08-818-111-70
Sequence 70, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David J.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-70

Query Match 54.4%; Score 37; DB 4; Length 344;
Best Local Similarity 77.8%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11
DB 106 AGTAPTAGD 114

RESULT 14
US-09-056-556-69
Sequence 69, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-69

Query Match 54.4%; Score 37; DB 4; Length 344;
Best Local Similarity 77.8%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11
DB 106 AGTAPTAGD 114

Db 106 AGTAPAGD 114

RESULT 15
US-09-072-596-70; Sequence 70, Application US/09072596
; Patent No. 6458366

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Campos-Neto, Antonia

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Twardzik, Daniel R.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Hendrickson, Ronald C.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

; NUMBER OF SEQUENCES: 350

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/072,596

; FILING DATE: 05-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.417C9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-072-596-70

Query Match 54.4%; Score 37; DB 4; Length 344;

Best Local Similarity 77.8%; Pred. No. 84;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPAGN 11

DB 106 AGTAPAGD 114

Search completed: February 6, 2004, 11:40:46

Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 11:39:31 ; Search time 34 Seconds

(without alignments)
80.058 Million cell updates/sec

Title: US-09-618-577-28

Perfect score: 68

Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-224-125-22	Sequence 22, App1
2	68	100.0	147	US-10-224-125-38	Sequence 38, App1
3	68	100.0	147	US-10-224-125-39	Sequence 39, App1
4	68	100.0	147	US-10-224-125-40	Sequence 40, App1
5	68	100.0	168	US-09-839-894-34	Sequence 34, App1
6	58	85.3	11	US-10-224-125-25	Sequence 25, App1
7	54	79.4	10	US-10-224-125-10	Sequence 10, App1
8	54	79.4	10	US-10-224-125-21	Sequence 21, App1
9	48	70.6	134	US-09-839-894-40	Sequence 40, App1
10	47	69.1	167	US-09-839-894-4	Sequence 4, App1
11	46	67.6	142	US-09-839-894-38	Sequence 38, App1
12	42	61.8	980	US-10-369-493-20514	Sequence 20514, A
13	41	60.3	8	US-10-224-125-20	Sequence 20, App1
14	41	60.3	179	US-10-001-245-213	Sequence 213, App
15	41	60.3	313	US-10-001-245-212	Sequence 212, App

16	40	58.8	362	12	US-10-374-780A-2098	Sequence 2098, Ap
17	40	58.8	510	12	US-10-369-493-4244	Sequence 4244, Ap
18	39	57.4	333	11	US-09-847-208-147	Sequence 147, App
19	39	57.4	333	12	US-10-001-245-189	Sequence 189, App
20	39	57.4	376	12	US-10-084-843-202	Sequence 202, App
21	39	57.4	376	12	US-10-193-002-197	Sequence 197, App
22	38	55.9	297	12	US-10-353-856-15	Sequence 15, App1
23	38	55.9	297	12	US-10-353-856-33	Sequence 33, App1
24	38	55.9	363	14	US-10-027-450-20	Sequence 20, App1
25	38	55.9	364	12	US-10-353-856-14	Sequence 14, App1
26	38	55.9	364	12	US-10-353-856-32	Sequence 32, App1
27	38	55.9	464	12	US-10-353-856-42	Sequence 42, App1
28	38	55.9	464	15	US-10-156-761-10151	Sequence 10151, A
29	38	55.9	676	10	US-09-337-946A-17	Sequence 17, App1
30	38	55.9	676	12	US-10-353-856-13	Sequence 13, App1
31	38	55.9	676	12	US-10-353-856-31	Sequence 31, App1
32	38	55.9	676	12	US-10-353-856-41	Sequence 41, App1
33	38	55.9	676	15	US-10-066-506A-12	Sequence 12, App1
34	38	55.9	747	15	US-10-066-506A-2	Sequence 2, App1
35	38	55.9	1079	11	US-09-820-843A-20	Sequence 20, App1
36	38	55.9	2037	15	US-10-184-644-591	Sequence 591, App
37	38	55.9	2037	15	US-10-184-634-591	Sequence 591, App
38	38	55.9	2700	12	US-10-140-472-27	Sequence 27, App1
39	38	55.9	2700	12	US-10-141-761-27	Sequence 27, App1
40	38	55.9	2700	12	US-10-142-885-27	Sequence 27, App1
41	38	55.9	2700	12	US-10-158-790-27	Sequence 27, App1
42	38	55.9	2700	12	US-10-137-871-27	Sequence 27, App1
43	38	55.9	2700	12	US-10-140-805-27	Sequence 27, App1
44	38	55.9	2700	12	US-10-140-864-27	Sequence 27, App1
45	38	55.9	2700	12	US-10-140-923-27	Sequence 27, App1

ALIGNMENTS

RESULT 1
US-10-224-125-22
Sequence 22, Application US/10224125
Publication No. US20030161889N1
GENERAL INFORMATION:
APPLICANT: REID, ROBERT H.
APPLICANT: BOEDERER, EDGAR C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SETTERSTROM, JEAN A.
APPLICANT: MCCOEN, CHARLES
APPLICANT: CASSELS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
FILE REFERENCE: ARMY 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/352,944
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: 08/034,949
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/867,301
PRIOR FILING DATE: 1992-04-10
PRIOR APPLICATION NUMBER: 07/805,721
PRIOR FILING DATE: 1991-11-21
PRIOR APPLICATION NUMBER: 07/690,485
PRIOR FILING DATE: 1991-04-24
PRIOR APPLICATION NUMBER: 07/521,945
PRIOR FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: 07/493,597
PRIOR FILING DATE: 1990-03-15
PRIOR APPLICATION NUMBER: 06/590,308
PRIOR FILING DATE: 1984-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-224-125-22

Query Match 100.0%; Score 68; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
Db 1 KTAGTAPTAGNYS 13

RESULT 2
US-10-224-125-38

Sequence 38, Application US/10224125
Publication No. US20030161889A1
GENERAL INFORMATION:

APPLICANT: REID, ROBERT H.
APPLICANT: BOEDEKER, EDGAR C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SETTERSTROM, JEAN A.
APPLICANT: MCOUEN, CHARLES
APPLICANT: CASSELS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
FILE REFERENCE: Army 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/352,944
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: 08/034,949
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/867,301
PRIOR FILING DATE: 1992-04-10
PRIOR APPLICATION NUMBER: 07/805,721
PRIOR FILING DATE: 1991-11-21
PRIOR APPLICATION NUMBER: 07/690,485
PRIOR FILING DATE: 1991-04-24
PRIOR APPLICATION NUMBER: 07/521,945
PRIOR FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: 07/493,597
PRIOR FILING DATE: 1990-03-15
PRIOR APPLICATION NUMBER: 06/590,308
PRIOR FILING DATE: 1984-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
TYPE: PRT
LENGTH: 147
ORGANISM: Macaca mulatta
US-10-224-125-38

Query Match 100.0%; Score 68; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
Db 124 KTAGTAPTAGNYS 136

RESULT 3
US-10-224-125-39

Sequence 39, Application US/10224125
Publication No. US20030161889A1

GENERAL INFORMATION:

APPLICANT: REID, ROBERT H.
APPLICANT: BOEDEKER, EDGAR C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SETTERSTROM, JEAN A.
APPLICANT: MCOUEN, CHARLES
APPLICANT: CASSELS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
FILE REFERENCE: Army 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/352,944
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: 08/034,949
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/867,301
PRIOR FILING DATE: 1992-04-10
PRIOR APPLICATION NUMBER: 07/805,721
PRIOR FILING DATE: 1991-11-21
PRIOR APPLICATION NUMBER: 07/690,485
PRIOR FILING DATE: 1991-04-24
PRIOR APPLICATION NUMBER: 07/521,945
PRIOR FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: 07/493,597
PRIOR FILING DATE: 1990-03-15
PRIOR APPLICATION NUMBER: 06/590,308
PRIOR FILING DATE: 1984-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
TYPE: PRT
LENGTH: 147
ORGANISM: Macaca mulatta
US-10-224-125-39

Query Match 100.0%; Score 68; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
Db 124 KTAGTAPTAGNYS 136

RESULT 4
US-10-224-125-40

Sequence 40, Application US/10224125
Publication No. US20030161889A1
GENERAL INFORMATION:

APPLICANT: REID, ROBERT H.
APPLICANT: BOEDEKER, EDGAR C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SETTERSTROM, JEAN A.
APPLICANT: MCOUEN, CHARLES
APPLICANT: CASSELS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
FILE REFERENCE: Army 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/352,944
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: 08/034,949
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/867,301
PRIOR FILING DATE: 1992-04-10

;; PRIOR APPLICATION NUMBER: 07/805,721
;; PRIOR FILING DATE: 1991-11-21
;; PRIOR APPLICATION NUMBER: 07/690,485
;; PRIOR FILING DATE: 1991-04-24
;; PRIOR APPLICATION NUMBER: 07/521,945
;; PRIOR FILING DATE: 1990-05-11
;; PRIOR APPLICATION NUMBER: 07/493,597
;; PRIOR FILING DATE: 1990-03-15
;; PRIOR APPLICATION NUMBER: 06/590,308
;; PRIOR FILING DATE: 1984-03-16
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 40
;; LENGTH: 147
;; TYPE: PRT
;; ORGANISM: Macaca mulatta
US-10-224-125-40

Query Match 100.0%; Score 68; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTACTAPTAGNYS 13
DB 124 KTACTAPTAGNYS 136

RESULT 5
US-09-839-894-34
;; Sequence 34, Application US/09839894
;; Patent No. US20020176868A1
;; GENERAL INFORMATION:
;; APPLICANT: Alldoun, Zeev
;; APPLICANT: Barry, Eileen M.
;; APPLICANT: Levine, Myron M.
;; APPLICANT: University of Maryland
;; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
;; FILE REFERENCE: UOFMD.006A
;; CURRENT APPLICATION NUMBER: US/09/839,894
;; CURRENT FILING DATE: 2001-04-20
;; PRIOR APPLICATION NUMBER: 60/198,626
;; PRIOR FILING DATE: 2000-04-20
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 34
;; LENGTH: 168
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: ETEC Protein Homology Sequence
US-09-839-894-34

Query Match 100.0%; Score 68; DB 10; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTACTAPTAGNYS 13
DB 145 KTACTAPTAGNYS 157

RESULT 6
US-10-224-125-25
;; Sequence 25, Application US/10224125
;; Publication No. US20030161889A1
;; GENERAL INFORMATION:
;; APPLICANT: REID, ROBERT H.
;; APPLICANT: BOEDEKER, EDGAR C.
;; APPLICANT: VAN HAMONT, JOHN
;; APPLICANT: SETTERSTROM, JEAN A.
;; APPLICANT: MCOUEEN, CHARLES
;; APPLICANT: CASELS, FREDERICK

;; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
;; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
;; FILE REFERENCE: Army 108
;; CURRENT APPLICATION NUMBER: US/10/224,125
;; CURRENT FILING DATE: 2002-08-20
;; PRIOR APPLICATION NUMBER: 08/789,734
;; PRIOR FILING DATE: 1997-01-27
;; PRIOR APPLICATION NUMBER: 08/352,944
;; PRIOR FILING DATE: 1994-12-09
;; PRIOR APPLICATION NUMBER: 08/034,949
;; PRIOR FILING DATE: 1993-03-22
;; PRIOR APPLICATION NUMBER: 07/867,301
;; PRIOR FILING DATE: 1992-04-10
;; PRIOR APPLICATION NUMBER: 07/805,721
;; PRIOR FILING DATE: 1991-11-21
;; PRIOR APPLICATION NUMBER: 07/690,485
;; PRIOR FILING DATE: 1991-04-24
;; PRIOR APPLICATION NUMBER: 07/521,945
;; PRIOR FILING DATE: 1990-05-11
;; PRIOR APPLICATION NUMBER: 07/493,597
;; PRIOR FILING DATE: 1990-03-15
;; PRIOR APPLICATION NUMBER: 06/590,308
;; PRIOR FILING DATE: 1984-03-16
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 25
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-224-125-25

Query Match 85.3%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13
DB 1 AGTAPTAGNYS 11

RESULT 7
US-10-224-125-10
;; Sequence 10, Application US/10224125
;; Publication No. US20030161889A1
;; GENERAL INFORMATION:
;; APPLICANT: REID, ROBERT H.
;; APPLICANT: BOEDEKER, EDGAR C.
;; APPLICANT: VAN HAMONT, JOHN
;; APPLICANT: SETTERSTROM, JEAN A.
;; APPLICANT: MCOUEEN, CHARLES
;; APPLICANT: CASELS, FREDERICK
;; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
;; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
;; FILE REFERENCE: Army 108
;; CURRENT APPLICATION NUMBER: US/10/224,125
;; CURRENT FILING DATE: 2002-08-20
;; PRIOR APPLICATION NUMBER: 08/789,734
;; PRIOR FILING DATE: 1997-01-27
;; PRIOR APPLICATION NUMBER: 08/352,944
;; PRIOR FILING DATE: 1994-12-09
;; PRIOR APPLICATION NUMBER: 08/034,949
;; PRIOR FILING DATE: 1993-03-22
;; PRIOR APPLICATION NUMBER: 07/867,301
;; PRIOR FILING DATE: 1992-04-10
;; PRIOR APPLICATION NUMBER: 07/805,721
;; PRIOR FILING DATE: 1991-11-21
;; PRIOR APPLICATION NUMBER: 07/690,485
;; PRIOR FILING DATE: 1991-04-24

; PRIOR APPLICATION NUMBER: 07/521,945
 ; PRIOR FILING DATE: 1990-05-11
 ; PRIOR APPLICATION NUMBER: 07/493,597
 ; PRIOR FILING DATE: 1990-03-15
 ; PRIOR APPLICATION NUMBER: 06/590,308
 ; PRIOR FILING DATE: 1984-03-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO: 10
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; US-10-224-125-10

Query Match 79.4%; Score 54; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGTAPTAGNY 12
 |||||
 Db 1 AGTAPTAGNY 10

RESULT 8
 ; US-10-224-125-21
 ; Sequence 21, Application US/107224125
 ; Publication No. US20030161869A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REID, ROBERT H.
 ; APPLICANT: BOEDEKER, EDGAR C.
 ; APPLICANT: VAN HAMONT, JOHN
 ; APPLICANT: SETTERSTROM, JEAN A.
 ; APPLICANT: MCOHEN, CHARLES
 ; APPLICANT: CASSLS, FREDERICK
 ; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
 ; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
 ; FILE REFERENCE: Army 108
 ; CURRENT APPLICATION NUMBER: US/10/224,125
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 08/789,734
 ; PRIOR FILING DATE: 1997-01-27
 ; PRIOR APPLICATION NUMBER: 08/352,944
 ; PRIOR FILING DATE: 1994-12-09
 ; PRIOR APPLICATION NUMBER: 08/034,949
 ; PRIOR FILING DATE: 1993-03-22
 ; PRIOR APPLICATION NUMBER: 07/867,301
 ; PRIOR FILING DATE: 1992-04-10
 ; PRIOR APPLICATION NUMBER: 07/805,721
 ; PRIOR FILING DATE: 1991-11-21
 ; PRIOR APPLICATION NUMBER: 07/690,485
 ; PRIOR FILING DATE: 1991-04-24
 ; PRIOR APPLICATION NUMBER: 07/521,945
 ; PRIOR FILING DATE: 1990-05-11
 ; PRIOR APPLICATION NUMBER: 07/493,597
 ; PRIOR FILING DATE: 1990-03-15
 ; PRIOR APPLICATION NUMBER: 06/590,308
 ; PRIOR FILING DATE: 1984-03-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO: 21
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; US-10-224-125-21

Query Match 79.4%; Score 54; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTAPTAGNYS 13
 |||||
 Db 1 GTAPTAGNYS 10

RESULT 9
 ; US-09-839-894-40
 ; Sequence 40, Application US/09839894
 ; Patent No. US20020176868A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altboum, Zeev
 ; APPLICANT: Barry, Eileen M.
 ; APPLICANT: Levine, Myron M.
 ; APPLICANT: University of Maryland
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
 ; FILE REFERENCE: CSA OPERON
 ; CURRENT APPLICATION NUMBER: US/09/839,894
 ; CURRENT FILING DATE: 2001-04-20
 ; PRIOR APPLICATION NUMBER: 60/198,626
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 40
 ; LENGTH: 134
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: ETEC Protein Homology Sequence
 ; US-09-839-894-40

Query Match 70.6%; Score 48; DB 10; Length 134;
 Best Local Similarity 81.8%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAGTAPTAGNY 12
 |||||
 Db 112 TGTAPTAGNY 122

RESULT 10
 ; US-09-839-894-4
 ; Sequence 4, Application US/09839894
 ; Patent No. US20020176868A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altboum, Zeev
 ; APPLICANT: Barry, Eileen M.
 ; APPLICANT: Levine, Myron M.
 ; APPLICANT: University of Maryland
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
 ; FILE REFERENCE: UOPMD.006A
 ; CURRENT APPLICATION NUMBER: US/09/839,894
 ; CURRENT FILING DATE: 2001-04-20
 ; PRIOR APPLICATION NUMBER: 60/198,626
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: E. coli
 ; US-09-839-894-4

Query Match 69.1%; Score 47; DB 10; Length 167;
 Best Local Similarity 75.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TAGTAPTAGNYS 13
 |||||

Db 145 TTAQAPTANYS 156

RESULT 11

US-09-839-894-38
; Sequence 38, Application US/09839894
; Patent No. US20020176868A1
; GENERAL INFORMATION:
; APPLICANT: Alboum, Zeev
; APPLICANT: Barry, Eileen M.
; APPLICANT: Levine, Myron M.
; APPLICANT: University of Maryland
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
; FILE REFERENCE: UOFPD.006A
; CURRENT APPLICATION NUMBER: US/09/839,894
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/198,626
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ETEC Protein Homology Sequence
US-09-839-894-38

Query Match 67.6%; Score 46; DB 10; Length 142;
Best Local Similarity 72.7%; Pred. No. 4.1;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGAPTAGNY 12

Db 113 TGTAPSNKTY 123

RESULT 12

US-10-369-493-20514
; Sequence 20514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20514
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Rhodospseudomonas palustris
US-10-369-493-20514

Query Match 61.8%; Score 42; DB 12; Length 980;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12

Db 864 AGTAPASGNF 873

RESULT 13

US-10-224-125-20

; Sequence 20, Application US/10224125
; Publication No. US20030161889A1
; GENERAL INFORMATION:
; APPLICANT: REID, ROBERT H.
; APPLICANT: BOEDEKER, EDGAR C.
; APPLICANT: VAN HAMONT, JOHN
; APPLICANT: SETTERSTROM, JEAN A.
; APPLICANT: MCCUEEN, CHARLES
; APPLICANT: CASSELS, FREDERICK
; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
; TITLE OF INVENTION: BIODEGRADABLE-BIOCOMPATIBLE MICROSPHERES
; FILE REFERENCE: Army 108
; CURRENT APPLICATION NUMBER: US/10/224,125
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 08/789,734
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 08/352,944
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: 08/034,949
; PRIOR FILING DATE: 1993-03-22
; PRIOR APPLICATION NUMBER: 07/867,301
; PRIOR FILING DATE: 1992-04-10
; PRIOR APPLICATION NUMBER: 07/805,721
; PRIOR FILING DATE: 1991-11-21
; PRIOR APPLICATION NUMBER: 07/690,485
; PRIOR FILING DATE: 1991-04-24
; PRIOR APPLICATION NUMBER: 07/521,945
; PRIOR FILING DATE: 1990-05-11
; PRIOR APPLICATION NUMBER: 07/493,597
; PRIOR FILING DATE: 1990-03-15
; PRIOR APPLICATION NUMBER: 06/590,308
; PRIOR FILING DATE: 1984-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-224-125-20

Query Match 60.3%; Score 41; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPT 8

Db 1 KTAGTAPT 8

RESULT 14

US-10-001-245-213
; Sequence 213, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens
; FILE REFERENCE: 4305/11942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213

LENGTH: 179
TYPE: PRT
ORGANISM: Hordeum vulgare
US-10-001-245-213

Query Match 60.3%; Score 41; DB 12; Length 179;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGTAPTAGNY 12
Db 168 AGAATAGNY 177

RESULT 15

US-10-001-245-212
Sequence 212, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: No. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 212
LENGTH: 313
TYPE: PRT
ORGANISM: Hordeum vulgare
US-10-001-245-212

Query Match 60.3%; Score 41; DB 12; Length 313;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGTAPTAGNY 12
Db 302 AGAATAGNY 311

Search completed: February 6, 2004, 11:45:13
Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:30 ; Search time 21 Seconds
(without alignments)
59.533 Million cell updates/sec

Title: US-09-618-577-28
Perfect score: 68
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	170	1 YOECC1	CPAI fimbrial prot
2	68	100.0	170	2 BE6617	colonic acid factor
3	46	67.6	359	2 S44738	C02C2.5 protein -
4	44	64.7	384	1 W2ML41	E2 protein - human
5	42	61.8	358	2 D83919	branched-chain ami
6	41	60.3	218	2 S29712	segmentation prote
7	41	60.3	313	2 JC5475	pollen allergen 9
8	41	60.3	560	2 S41808	glucose-6-phosphat
9	40	58.8	346	2 T51728	hypothetical prote
10	40	58.8	792	2 T26050	hypothetical prote
11	39	57.4	1791	2 T02345	hypothetical prote
12	39	57.4	212	2 BE9522	hypothetical prote
13	39	57.4	256	2 T03371	glycine-rich prote
14	39	57.4	306	2 D70924	probable cdkc prot
15	39	57.4	333	2 A39098	allergen Poa p IX
16	39	57.4	333	2 A39098	hypothetical prote
17	38	55.9	124	1 VGLJ51	trans-regulatory s
18	38	55.9	161	2 G72711	hypothetical prote
19	38	55.9	321	1 R5UBP0	acidic ribosomal p
20	38	55.9	343	2 R82755	transcription regu
21	38	55.9	363	2 S57763	branched-chain ami
22	38	55.9	430	2 JC4720	toxin co-regulated
23	38	55.9	723	2 T14765	hypothetical glyci
24	38	55.9	1079	2 B70807	hypothetical glyci
25	37	54.4	153	2 C72420	hypothetical prote
26	37	54.4	180	2 B83064	hypothetical prote
27	37	54.4	197	2 F75468	probable DNA polym
28	37	54.4	231	1 D64170	hypothetical prote
29	37	54.4	262	2 C71109	hypothetical prote

30	37	54.4	344	2 C70580	hypothetical prote
31	37	54.4	793	2 H82594	feric enterobacti
32	37	54.4	1145	2 T18235	transcription acti
33	37	54.4	1557	2 T28811	hypothetical prote
34	37	54.4	1787	2 AG1360	probable tape-meas
35	37	54.4	1788	2 AH1447	probable tape-meas
36	37	54.4	1815	2 B95942	conserved hypotet
37	36	52.9	53	2 S18013	protein-tyrosine k
38	36	52.9	153	2 JQ0139	hypothetical 17.8k
39	36	52.9	257	2 G36810	hypothetical prote
40	36	52.9	261	2 D75335	hypothetical prote
41	36	52.9	310	2 B73476	conserved hypotet
42	36	52.9	352	2 S16547	neutral proteinase
43	36	52.9	356	2 H69750	branched-chain ami
44	36	52.9	390	2 G82844	cysteine synthase
45	36	52.9	415	2 A35560	lysosomal membrane

ALIGNMENTS

RESULT 1
YOECC1
CPAI fimbrial protein precursor - Escherichia coli
N/Alternate names: CPAI pilin; colonization factor antigen I (CPAI)
C/Species: Escherichia coli
C/Date: 14-Nov-1993 #sequence revision 30-Jun-1991 #text_change 15-Nov-1996
A/Accession: A30589; A03495; A43831
R/Karjalainen, T.K.; Evans, D.G.; So, M.; Lee, C.H.
Infect. Immun. 57, 1126-1130, 1989
A/Title: Molecular cloning and nucleotide sequence of the colonization factor antigen I
A/Reference number: A30589; MUID:89173309; PMID:2564374
A/Accession: A30589
A/Molecule type: DNA
A/Residues: 1-170 <KAR>
R/Klemp, P.
Eur. J. Biochem. 124, 339-348, 1982
A/Title: Primary structure of the CPAI fimbrial protein from human enterotoxigenic Esche
A/Reference number: A03495; MUID:82235736; PMID:6124420
A/Accession: A03495
A/Molecule type: DNA
A/Residues: 24-75, 'N', 77-96, 'A', 98-170 <KLE>
A/Experimental source: strain H10407
R/Cassels, F.J.; Deal, C.D.; Reid, R.H.; Jarboe, D.L.; Naus, J.L.; Carter, J.M.; Boedeke
Infect. Immun. 60, 2174-2181, 1992
A/Title: Analysis of Escherichia coli colonization factor antigen I linear B-cell epitope
A/Reference number: A43831; MUID:92267624; PMID:1375193
A/Accession: A43831
A/Molecule type: protein
A/Residues: 24-170 <CAS>
A/Experimental source: strain H10407
A/Note: Sequence extracted from NCBI backbone (NCBIP:104220)
C/Comment: The CPAI fimbriae are rather rigid, thread-like filaments of 0.5-1 micrometer,
tical protein subunits.
C/Superfamily: CPAI fimbrial protein
C/Keywords: fimbria
F:1-23/Domin: signal sequence #status predicted <SIG>
F:24-170/Product: CPAI fimbrial protein #status experimental <MAT>
Query Match 100.0%; Score 68; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KTAGTAPTAGNYS 13
DB 147 KTAGTAPTAGNYS 159
RESULT 2
BE6617
colonic acid factor antigen I precursor - Escherichia coli plasmid NTP113
C/Species: Escherichia coli
C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-May-1996

C:Accession: B56617
 R:Jordi, B.T.; Willehaw, G.A.; van der Zeijst, B.A.; Gaaststra, W.
 DNA Seq. 2, 257-263, 1992
 A>Title: The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of hu
 A:Reference number: A56617; MUID:92329981; PMID:1352712
 A:Accession: B56617
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-170 <OR>
 A:Experimental source: enterotoxigenic strain, CFA/I-ST plasmid NTP13
 A>Note: sequence inconsistent with nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:108960, NCBI:108970)
 C:Genetics:
 A:Gene: cfab
 A:Genome: plasmid
 C:Superfamily: CFAI fimbrial protein

Query Match 100.0%; Score 68; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
 Db 147 KTAGTAPTAGNYS 159

RESULT 3
 S44738
 C02C2.5 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 08-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
 C:Accession: S44738
 R:Wilson, R.
 Submitted to the EMBL Data Library, September 1993
 A:Description: Sequence of the C. elegans cosmid C02C2.
 A:Reference number: S44738
 A:Accession: S44738
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <NUL>
 A:Cross-references: EMBL:123649; NID:g388566; PID:g388568
 C:Genetics:
 A:Introns: 69/3; 101/3; 127/3; 178/1; 219/2; 252/3; 313/1

Query Match 67.6%; Score 46; DB 2; Length 359;
 Best Local Similarity 72.7%; Pred. No. 2.2;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGN 11
 Db 175 KTAGTSPSVGN 185

RESULT 4
 W2ML41
 E2 protein - human papillomavirus type 41
 C:Species: human papillomavirus type 41
 A>Note: host Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Feb-1997
 C:Accession: D43550
 R:Hirt, L.; Hirsch-Benam, A.; De Villiers, E.M.
 Virus Res. 18, 179-190, 1990
 A>Title: Nucleotide sequence of human papillomavirus (HPV) type 41: an unusual HPV type
 A:Reference number: A43550
 A:Accession: D43550
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-384 <HIR>
 A:Cross-references: EMBL:X56147
 C:Superfamily: papillomavirus E2 protein
 A:Keywords: DNA binding; early protein; transcription regulation
 Query Match 64.7%; Score 44; DB 1; Length 384;

Best Local Similarity 66.7%; Pred. No. 5.3;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 12
 Db 291 KTAGVAPAEGHY 302

RESULT 5
 B83919
 branched-chain amino acid aminotransferase bcat [imported] - Bacillus halodurans (strain
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fujii, F.; Hiran
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83919
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STO>
 A:Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PID:BA05875.1; GSPDB:GN001
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: bcat
 C:Superfamily: branched-chain-amino-acid transaminase BAT1

Query Match 61.8%; Score 42; DB 2; Length 358;
 Best Local Similarity 80.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTAPTAGNYS 13
 Db 194 GTATGNGYS 203

RESULT 6
 S29712
 segmentation protein hairy - red flour beetle
 C:Species: Tribolium castaneum (red flour beetle)
 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
 C:Accession: S29712
 R:Sommer, R.J.; Tautz, D.
 Nature 361, 448-450, 1993
 A>Title: Involvement of an orthologue of the Drosophila pair-rule gene hairy in segment
 A:Reference number: S29712; MUID:93156810; PMID:8429884
 A:Accession: S29712
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <SOM>

Query Match 60.3%; Score 41; DB 2; Length 218;
 Best Local Similarity 61.5%; Pred. No. 9.9;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
 Db 169 KTASTASASNYS 181

RESULT 7
 JCS475
 pollen allergen 9 precursor - barley
 N:Alternate names: Hor v 9
 C:Species: Hordeum vulgare (barley)
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Aug-1999
 C:Accession: JCS475
 R:Aswood, J.D.; Hill, R.D.
 Gene 182, 53-62, 1996
 A>Title: Cloning and expression pattern of Hor v 9, the group 9 pollen isoallergen from
 A:Reference number: JCS475; MUID:97136690; PMID:8982067
 A:Accession: JCS475

A:Molecule type: mRNA
A:Residues: 1-313 <AST>
A:Cross-references: GB:U57845; NID:G1808986; PIDN:AA41585.1; PID:G1808987
C:Comment: This protein belongs to group 9 pollen allergen.
C:Superfamily: grass pollen allergen IX
F1-27/Domain: signal sequence #status predicted <SIG>
F1-28-313/Domain: pollen allergen #status predicted <MAT>
F1-290-309/Domain: transmembrane #status predicted <TM>

Query Match 60.3%; Score 41; DB 2; Length 313;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12
|||
Db 302 AGAATAGNY 311

RESULT 8
S41808
glucose-6-phosphate isomerase (EC 5.3.1.9), cytosolic - Arabidopsis thaliana
N:Alternate names: phosphoglucose isomerase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S41808
R:Thomas, B.R.; Ford, V.S.; Pichersky, E.; Gottlieb, L.D.
Genetics 135, 895-905, 1993
A>Title: Molecular characterization of duplicate cytosolic phosphoglucose isomerase gene
A:Reference number: S41806; MUID:94123980; PMID:823986
A:Accession: S41808
A:Molecule type: DNA
A:Residues: 1-560 <THO>
A:Cross-references: EMBL:X69195; NID:G415922; PIDN:CAA48940.1; PID:G415923
C:Genetics:
A:Gene: pgic
A:Introns: 18/3; 44/2; 71/3; 87/3; 139/3; 172/1; 186/2; 209/1; 237/2; 253/3; 278/1; 298/
C:Superfamily: glucose-6-phosphate isomerase
C:Keywords: cytosol; gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomere

Query Match 60.3%; Score 41; DB 2; Length 560;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNY 13
:|||||
Db 531 RTGTAPEGFNYS 543

RESULT 9
T51728
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51728
R:Olney, M.A.; Briggs, W.R.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana mRNA of unknown function.
A:Reference number: Z25441
A:Accession: T51728
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-346 <OLN>
A:Cross-references: EMBL:AF087435; PIDN:AAD11574.1
A:Experimental source: cultivar Columbia

Query Match 58.8%; Score 40; DB 2; Length 346;
Best Local Similarity 72.7%; Pred. No. 24;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGN 11
|||||
Db 304 KTAGPAPTYGH 314

RESULT 10
T26050
hypothetical protein W01C9.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26050
R:Sim, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20143
A:Accession: T26050
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-792 <WIL>
A:Cross-references: EMBL:Z49969; PIDN:CAA90267.1; GSPDB:GN00020; CESP:W01C9.3
A:Experimental source: clone W01C9
C:Genetics:
A:Gene: CESP:W01C9.3
A:Map position: 2
A:Introns: 15/1; 40/1; 66/3; 101/3; 182/2; 270/3; 338/3; 366/1; 597/3; 613/2; 646/2; 684/
Query Match 58.8%; Score 40; DB 2; Length 792;
Best Local Similarity 58.3%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNY 12
:|||||
Db 251 QTAGSPPIKGY 262

RESULT 11
T02345
hypothetical protein KIAA0324 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C:Accession: T02345
R:Rickey, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.;
re, J.; White, S.; Beng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.
submitted to the EMBL Data Library, March 1998
A:Description: Sequencing of human chromosome 16p13.3.
A:Reference number: Z14664
A:Accession: T02345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1791 <RIC>
A:Cross-references: EMBL:AC004493; NID:G2396648; PIDN:AAC08453.1; PID:G2396650
C:Genetics:
A:Map position: 16
A:Introns: 1610/2; 1706/2
A:Note: KIAA0324

Query Match 58.8%; Score 40; DB 2; Length 1791;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12
:|||||
Db 1346 SGTPTTANY 1355

RESULT 12
BE9522
hypothetical protein AF2181 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: BE9522
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artich, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: E69522
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-212 <KLE>
 A:Cross-references: GB:AE000954; GB:AE000782; NID:g2689277; PIDN:AA89076.1; PID:g264834

Query Match 57.4%; Score 39; DB 2; Length 212;
 Best Local Similarity 72.7%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13
 DB 132 AGAALAGNYS 142

RESULT 13

T03371
 glycine-rich protein grp3 - maize

C:Species: Zea mays (maize)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T03371

R:Godeffroy, M.L.; Muller, D.; Felix, G.

Plant Mol. Biol. 36: 799-802, 1998

A:Title: Root-specific expression of a Zea mays gene encoding a novel glycine-rich protein

A:Reference number: Z14904; MUID:98187261; PMID:9526513

A:Accession: T03371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-256 <GOD>

A:Cross-references: EMBL:Y07781; NID:g1532070; PIDN:CA69104.1; PID:g1532071

A:Experimental source: strain DK105; root

C:Genetics:

A:Gene: grp3

C:Superfamily: glycine-rich cell wall structural protein 1

Query Match 57.4%; Score 39; DB 2; Length 256;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNYS 13
 DB 114 TAAGPSSGNVA 125

RESULT 14

D70924

probable cda protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: D70924

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feltyell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70924

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <COL>

A:Cross-references: GB:Z74024; GB:AL123456; NID:g1250700; PIDN:CA98357.1; PID:g1403401

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: cda

C:Superfamily: phosphatidate cytidyltransferase

Query Match 57.4%; Score 39; DB 2; Length 306;
 Best Local Similarity 63.6%; Pred. No. 31;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12

DB 135 TTGAPSPGNV 145

RESULT 15

A39098

allergen Poa p IX (clone 41) - Kentucky bluegrass

C:Species: Poa pratensis (Kentucky bluegrass)

C:Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 20-Aug-1999

C:Accession: A39098

R:Silvanovich, A.; Astwood, J.; Zhang, L.; Olsen, E.; Kistl, F.; Sehon, A.; Mohapatra, S.

J. Biol. Chem. 266, 1204-1210, 1991

A:Title: Nucleotide sequence analysis of three cDNAs coding for Poa p IX isoallergens of

A:Reference number: A39098; MUID:91093232; PMID:1702432

A:Accession: A39098

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-333 <SLI>

A:Cross-references: GB:M38343; NID:g169628; PIDN:AA63456.1; PID:g169629

A>Note: the authors translated the codon GCG for residue 296 as Ser

C:Superfamily: grass pollen allergen IX

C:Keywords: pollen

Query Match 57.4%; Score 39; DB 2; Length 333;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNY 12
 DB 320 KTGAATPTAGGY 331

Search completed: February 6, 2004, 11:39:25
 Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:30; Search time 11 Seconds
(without alignments)
55.577 Million cell updates/sec

Title: US-09-618-577-28

Percent score: 68
Sequence: 1 KTACTGAPTACNYS 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	170	1	FMCI_ECOLI
2	46	67.6	359	1	YKH5_CABEL
3	44	64.7	387	1	VE2_HPV41
4	41	60.3	560	1	G6P1_ARATH
5	39	57.4	212	1	YL81_ARCFU
6	39	57.4	306	1	CDSA_MYCTU
7	39	57.4	330	1	A85B_MYCSC
8	39	57.4	333	1	MP92_POAPR
9	38	55.9	124	1	REV_STVCZ
10	38	55.9	321	1	PLA0_CHERU
11	38	55.9	362	1	ILVE_BACSV
12	38	55.9	364	1	VSGP_EBOBC
13	38	55.9	364	1	VSGP_EBOGA
14	38	55.9	364	1	VSGP_EBOZM
15	38	55.9	430	1	TCPB_VIBCH
16	38	55.9	676	1	VGP_EBOEC
17	38	55.9	676	1	VGP_EBOG4
18	38	55.9	676	1	VGP_EBOZ5
19	38	55.9	676	1	VGP_EBOZM
20	37	54.4	231	1	YOHK_HAEIN
21	37	54.4	1535	1	LMJ1_CABEL
22	36	52.9	257	1	VG45_HSVSA
23	36	52.9	352	1	NP11_ASFOR
24	36	52.9	356	1	YBGE_BACSU
25	36	52.9	415	1	LMF2_MOUSE
26	36	52.9	480	1	TGN2_HUMAN
27	36	52.9	521	1	IMH3_CANAL
28	36	52.9	666	1	FLID_VIBCH
29	36	52.9	717	1	ARA_DROME
30	36	52.9	769	1	ZBR2_CHICK
31	36	52.9	929	1	SPB3_YEAST
32	36	52.9	936	1	CAP1_RHOPA
33	36	52.9	1620	1	ALK_HUMAN

34	36	52.9	5703	1	MUSEB_HUMAN	Q9hce4 homo sapien
35	35.5	52.2	513	1	COX1_HUMAN	P00395 homo sapien
36	35.5	52.2	514	1	COX1_PONDA	P92692 pongo pygma
37	35	51.5	363	1	ALFB_CHICK	P07341 gallus galli
38	35	51.5	372	1	VSGP_EBOBS	O89455 ebola virus
39	35	51.5	401	1	P39_BRUBA	O06875 bruceella ab
40	35	51.5	482	1	T2EA_YEAST	P36100 saccharomyc
41	35	51.5	511	1	AMYC_HUMAN	P19961 homo sapien
42	35	51.5	511	1	AMYP_HUMAN	P04746 homo sapien
43	35	51.5	511	1	AMYS_HUMAN	P04745 homo sapien
44	35	51.5	540	1	PLIF_BRUBA	O52069 bruceella ab
45	35	51.5	547	1	MUTL_DEIRA	Q9rtt0 deinococcus

ALIGNMENTS

RESULT 1
FMCI_ECOLI STANDARD; PRT; 170 AA.
ID FMCI_ECOLI
AC P02971;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CFA/I fimbrial subunit B precursor (Colonization factor antigen I subunit B) (CFA/I pili) (CFA/I antigen).
GN CPAB.
OS Escherichia coli.
OC Plasmid NTP513.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89173309; PubMed=2564374;
RA Karjalainen T.K., Evans D.G., So M., Lee C.-H.;
RT "Molecular cloning and nucleotide sequence of the colonization factor antigen I gene of Escherichia coli.";
RL Infect. Immun. 57:1126-1130(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89330163; PubMed=2569152;
RA Hamers A.M., Pel H.J., Wilshaw G.A., Kusters J.G.,
RA van der Zeijst B.A.M., Gaastra W.;
RT "The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";
RL Microb. Pathog. 6:297-309(1989).
RN [3]
RP SEQUENCE OF 24-170 FROM N.A.
RX STRAIN=O78:H11 / H10407;
RC MEDLINE=82235736; PubMed=6124420;
RA Klemm P.;
RT "Primary structure of the CFA/I fimbrial protein from human enterotoxigenic Escherichia coli strains.";
RL Eur. J. Biochem. 124:339-348(1982).
RN [4]
RP SEQUENCE OF 24-42.
RX STRAIN=O78:H11 / H10407;
RC MEDLINE=90036735; PubMed=2572583;
RA Hall R.H., Maneval D.R. Jr., Collins J.H., Theibert J.L.,
RA Levine M.M.;
RT "Purification and analysis of colonization factor antigen I, coli surface antigen 1, and coli surface antigen 3 fimbriae from enterotoxigenic Escherichia coli.";
RL J. Bacteriol. 171:6372-6374(1989).
RN [5]
RP FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC - SUBUNIT: CFA/I FIMBRIAE ARE RATHER RIGID, THREAD-LIKE FILAMENTS OF 0.5-1 MICROMETER, WITH AN APPARENT AXIAL HOLE, AND A DIAMETER OF 7 NANOMETERS. A SINGLE CFA/I FIMBRIA CONSISTS OF ABOUT 100 IDENTICAL PROTEIN SUBUNITS.

```

CC -1- INDUCTION: CFA/I FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF
CC THE POSITIVE REGULATOR CFAD.
CC -1- SIMILARITY: TO THE CSI FIMBRIAL SUBUNIT A (CSOA).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M55661; AAC41415.1; -.
CC PIR: A30589; YOECC1.
CC Pfam: PF04449; Fimbrial_CSI; 1.
CC Fimbrin; Antigen; Plasmid; Signal.
CC SIGNAL
CC FT CHAIN 1 23
CC FT CONFLICT 24 170 CFA/I FIMBRIAL SUBUNIT B.
CC FT CONFLICT 37 37 V -> A (IN REF. 2).
CC FT CONFLICT 76 76 D -> N (IN REF. 3).
CC FT CONFLICT 97 97 S -> A (IN REF. 3).
CC SEQUENCE 170 AA; 17461 MW; 92434707F33CDAB CRC64;
CC
CC Query Match 100.0%; Score 68; DB 1; Length 170;
CC Best Local Similarity 100.0%; Pred. No. 7.7e-05;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 KTAGTAPTAGNY 13
CC DB 147 KTAGTAPTAGNY 159
CC
CC RESULT 2
CC YKHS CAEBL
CC ID YKHS CAEBL STANDARD; PRT; 359 AA.
CC AC P34273;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Hypothetical protein C02C2.5 in chromosome III.
CC GN C02C2.5
CC OS Caenorhabditis elegans.
CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC OC Rhabditidae; Peloderae; Caenorhabditis.
CC OX NCBI_TaxId=6239;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Bristol N2;
CC RX MEDLINE=94150718; PubMed=7906398;
CC RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
CC RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
CC RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
CC RA Fulton L., Garner A., Green P., Hawkins T., Hillier L., Jier M.,
CC RA Johnston L., Jones M., Kershaw J., Kirschen J., Laister N.,
CC RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
CC RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
CC RA Sims M., Smalton N., Smith A., Smith K., Sonhammer E., Staden R.,
CC RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
CC RA Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J.,
CC RA Wohlschlag P.;
CC RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
CC elegans.";
CC RL Nature 368:32-38(1994).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L23649; AAA27908.1; -.

```

```

DR PIR: S44738; S44738.
DR WormPep; C02C2.5; CE00031.
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
DR KW Hypothetical protein.
DR SEQUENCE 359 AA; 41326 MW; ECC9450C72FFB7B0 CRC64;
DR
DR Query Match 67.6%; Score 46; DB 1; Length 359;
DR Best Local Similarity 72.7%; Pred. No. 1;
DR Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
DR
DR QY 1 KTAGTAPTAGN 11
DR DB 175 KTAGTAPSEVN 185
DR
DR RESULT 3
DR VE2 HPV41
DR ID VE2 HPV41 STANDARD; PRT; 387 AA.
DR AC P27552;
DR DT 01-AUG-1992 (Rel. 23, Created)
DR DT 01-AUG-1992 (Rel. 23, Last sequence update)
DR DT 15-JUL-1998 (Rel. 35, Last annotation update)
DR DE Regulatory protein E2.
DR GN E2.
DR OS Human papillomavirus type 41.
DR OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
DR OC Papillomavirus.
DR OX NCBI_TaxId=10589;
DR RN [1]
DR RP SEQUENCE FROM N.A.
DR RX MEDLINE=91253264; PubMed=1645904;
DR RA Hirt L., Hirsch-Behnam A., de Villiers E.M.;
DR RT "Nucleotide sequence of human papillomavirus (HPV) type 41: an
DR RT unusual HPV type without a typical E2 binding site consensus
DR RT sequence.";
DR RL Virus Res. 18:119-190(1991).
CC -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNNGGT-3') PRESENT
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING ON E2RE'S POSITION
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC REPLICATION.
CC -1- SUBUNIT: Binds DNA as a dimer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X56147; CAA39615.1; -.
CC PIR: DA3550; W2WL41.
CC DR InterPro; IPR000427; E2_C.
CC DR InterPro; IPR001866; E2_N.
CC DR Pfam; PF00511; E2_C; 1.
CC DR Pfam; PF00508; E2_N; 1.
CC DR Pfam; PF00672; E2_C; 1.
CC DR Pfam; PF00678; E2_N; 1.
CC DR Problem; PD000678; E2_C; 1.
CC DR Problem; PD000678; E2_N; 1.
CC DR Early protein; Transcription regulation; Activator; DNA-binding;
CC DR Trans-acting factor; DNA replication; Repressor; Nuclear protein.
CC KW Trans-acting factor.
CC SEQUENCE 387 AA; 44230 MW; 8F9AAAC0395DBE48 CRC64;
CC
CC Query Match 64.7%; Score 44; DB 1; Length 387;
CC Best Local Similarity 66.7%; Pred. No. 2.5;
CC Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 KTAGTAPTAGNY 12

```


Db 294 KTACGAPBEGHY 305

RESULT 4

G6PI_ARATH STANDARD; PRT; 560 AA.
 AC P34795; Q9FE90; Q9FXM6; Q9FXM7; Q9FXM8; Q9FXM9; Q9FXN0; Q9FXN1;
 AC Q9FXN2; Q9FXN3; Q9FXN4; Q9FXN5;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 26-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI)
 DB (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI).
 GN PGIC OR AT5G42740 OR MJB21.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94123980; PubMed=8293986;
 RA Thomas B.R., Ford V.S., Pichersky E., Gottlieb L.D.;
 RT "Molecular characterization of duplicate cytosolic phosphoglucose
 RT isomerase genes in *Clarkia* and comparison to the single gene in
 RT *Arabidopsis*.";
 RL Genetics 135:895-905 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Many cultivars;
 RA Kawabe A., Yamane K., Miyashita N.T.;
 RT "DNA polymorphism at the cytosolic phosphoglucose isomerase (Pgic)
 RT locus of the wild plant *Arabidopsis thaliana*.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:401-414 (1997).
 RL -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
 RL phosphate.
 CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- POLYMORPHISM: Was sequenced in many cultivars; Ag-0, Bl-1, Bus-1,
 CC Cl-0, Cvi-0, Dra-0, Edi-0, Han-0, Hiroshima, In-0, Ita-0, Kas-1,
 CC Mr-0, Nkr-4, Ost-0, Pog-0, Rou-0, Su-0, Ts-1 and ws-0.
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X69195; CAA48940.1; -
 DR EMBL; AB044948; BAB17635.1; -
 DR EMBL; AB044949; BAB17636.1; -
 DR EMBL; AB044950; BAB17637.1; -
 DR EMBL; AB044951; BAB17638.1; -
 DR EMBL; AB044952; BAB17639.1; -
 DR EMBL; AB044953; BAB17640.1; -
 DR EMBL; AB044954; BAB17641.1; -
 DR EMBL; AB044955; BAB17642.1; -

DR EMBL; AB044956; BAB17643.1; -
 DR EMBL; AB044957; BAB17644.1; -
 DR EMBL; AB044958; BAB17645.1; -
 DR EMBL; AB044959; BAB17646.1; -
 DR EMBL; AB044960; BAB17647.1; -
 DR EMBL; AB044961; BAB17648.1; -
 DR EMBL; AB044962; BAB17649.1; -
 DR EMBL; AB044963; BAB17650.1; -
 DR EMBL; AB044964; BAB17651.1; -
 DR EMBL; AB044965; BAB17652.1; -
 DR EMBL; AB044966; BAB17653.1; -
 DR EMBL; AB044967; BAB17654.1; -
 DR EMBL; AB007647; BAB10650.1; -
 DR HSSP; Q9N1E2; IH0X.
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; PGI_1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Gluconeogenesis; Glycolysis; Isomerase; Polymorphism.
 FT ACT_SITE 392 392
 FT ACT_SITE 517 517
 FT VARIANT 3 3
 FT VARIANT 5 5
 FT VARIANT 36 36
 FT VARIANT 73 73
 FT VARIANT 95 95
 FT VARIANT 99 99
 FT VARIANT 105 105
 FT VARIANT 114 114
 FT VARIANT 119 119
 FT VARIANT 198 198
 FT VARIANT 295 295
 FT VARIANT 355 355
 FT VARIANT 425 425
 FT VARIANT 431 431
 FT VARIANT 432 432
 FT VARIANT 528 528
 SQ SEQUENCE 560 AA; 61717 MW; C4F5C7D8FE5F193B CRC64;
 Query Match 60.3%; Score 41; DB 1; Length 560;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Cy 1 KTACTAPTACGYS 13
 Db 531 RTGTAPEGFGYS 543
 RESULT 5
 ID YL81_ARCFU STANDARD; PRT; 212 AA.
 AC Y28102;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein AF2181.
 GN AF2181.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 CC NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klank H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerevage A.R., Graham D.E., Kyprides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kitzies E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weisman J.F., McDonald L., Uterback T.,
 Cotton M.D., Spriggs T., Arlisch P., Kaine B.P., Sykes S.M.,
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Weiss C.R.,
 Venter J.C.,
 "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon *Archaeoglobus fulgidus*.";
 Nature 390:364-370(1997).

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; AE000954; AAB89076.1; -;
 PIR; E69522; E69522.
 TIGR; AF2181; -;
 Hypothetical protein; Complete proteome.
 KMW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 212 AA; 24115 MW; 15371825122DEBD CRC64;

 Query Match 57.4%; Score 39; DB 1; Length 212;
 Best Local Similarity 72.7%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 AGTAPTAGNYS 13
 Db 132 AGAALAGNYS 142

 RESULT 6
 CDS MYCTU STANDARD; PRT; 306 AA.
 ID CDS MYCTU STANDARD; PRT; 306 AA.
 AC 010607;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphatidate cytidyltransferase (EC 2.7.7.41) (CDP-diacylglycerol
 synthetase) (CDP-diacylglyceride pyrophosphorylase) (CDP-diacylglycerol
 synthase) (CDP-phosphatidate cytidyltransferase) (CDP-DAG
 synthase) (CDP-DG synthetase).
 GN CDS OR RV2881C OR MT2948 OR MTCY274.12C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 CC
 OK NCBI_TaxId=1773;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eigleier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 Hornsby T., Jagsen K., Kroch A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares K.,
 Sulten J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN
 RN SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";

Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-
 CC diacylglycerol.
 CC -1- PATHWAY: Phospholipid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE CDS FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; Z74024; CA98357.1; -;
 PIR; AE007118; AAK47273.1; ALT_INIT.
 DR PIR; D70924; D70924.
 DR TIGR; MT2948; -;
 DR Tuberculin; RV2881C; -;
 DR InterPro: IPR000374; PCTransf.
 DR Pfam: PF01148; CTP_transf_1; 1.
 DR PROSITE: PS01315; CDS; 1.
 KW Transferase; Nucleotidyltransferase; Phospholipid biosynthesis;
 KW Transmembrane; Complete proteome.
 FT TRANSMEM 36 56 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 151 171 POTENTIAL.
 FT TRANSMEM 180 200 POTENTIAL.
 FT TRANSMEM 218 238 POTENTIAL.
 FT TRANSMEM 241 261 POTENTIAL.
 FT TRANSMEM 285 305 POTENTIAL.
 SQ SEQUENCE 306 AA; 32035 MW; 8FA81A108035099F CRC64;

 Query Match 57.4%; Score 39; DB 1; Length 306;
 Best Local Similarity 63.6%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 TAGAPTAGNY 12
 Db 135 TTGAPSPGNY 145

 RESULT 7
 A85B MYCSC STANDARD; PRT; 330 AA.
 ID A85B MYCSC STANDARD; PRT; 330 AA.
 AC 050397;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
 complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
 DE (Fibronectin-binding protein B).
 GN FBPB.
 OS Mycobacterium scrofulaceum.
 OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 CC
 OK NCBI_TaxId=1783;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19981;
 MEDLINE=9433707; PubMed=8047837;
 RA Takano M., Ohara N., Mizuno A., Yamada T.;
 RT "Cloning, sequencing and expression in *Escherichia coli* of the gene
 RT for alpha antigen from Mycobacterium scrofulaceum.";
 RL Scand. J. Immunol. 40:165-170(1994).
 CC -1- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
 CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
 CC MYCOXYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
 CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
 CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

```

CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C.GLUTAMICUM PSI PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D26187; BAA05332.1; -.
DR HSSP; P31953; 1DQY.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Transferrase; Acyltransferase; Antigen; Signal.
FT SIGNAL 1 40
FT CHAIN 1 40
FT ACT SITE 166 166 BY SIMILARITY.
FT ACT SITE 270 270 BY SIMILARITY.
FT ACT SITE 302 302 BY SIMILARITY.
SQ SEQUENCE 330 AA; 34943 MW; 09D6B04B5B9ED221 CRC64;

Query Match 57.4%; Score 39; DB 1; Length 330;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 3 AGTAPTAGNYS 13
DB 32 AGGAPTAGAFS 42

RESULT 8
MP92_POAPR
ID_MP92_POAPR STANDARD; PRT; 333 AA.
AC P22285;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Pollen allergen KBG 41 precursor (Pollen allergen Poa p 9) (Poa p IX).
OS Pollen allergen (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=91093332; PubMed=1702432;
RA Silvanovich A., Astwood J., Zhang L., Olsen E., Kisil F.T.,
RA Sehon A.H., Mohapatra S.S., Hill R.D.;
RT "Nucleotide sequence analysis of three cDNAs coding for Poa p IX
RT isoallergens of Kentucky bluegrass pollen.";
RL J. Biol. Chem. 266:1204-1210(1991).
[2]
RN CHARACTERIZATION.
RP MEDLINE=91268549; PubMed=2051020;
RA Olsen E., Zhang L., Hill R.D., Kisil F.T., Sehon A.H., Mohapatra S.S.;
RT "Identification and characterization of the Poa p IX group of basic
RT allergens of Kentucky bluegrass pollen.";
RL J. Immunol. 147:205-211(1991).
CC -1- TISSUE SPECIFICITY: POLLEN.
CC -1- MISCELLANEOUS: ITS C-TERMINUS MIGHT BE MEMBRANE-ASSOCIATED.
CC -1- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

DR EMBL; M38343; AAA63456.1; -.
DR PIR; A39098; A39098.
DR InterPro; IPR001778; POA_allergenc.
DR InterPro; IPR002914; POA_allergenN.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POAALLERGEN.
KW Allergen; Signal; Multigene family; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 333
FT DOMAIN 309 332 2 X 12 AA TANDEM REPEATS.
FT REPEAT 309 320 1.
FT REPEAT 321 332 2.
SQ SEQUENCE 333 AA; 32661 MW; 1FA48168C1334CA0 CRC64;

Query Match 57.4%; Score 39; DB 1; Length 333;
Best Local Similarity 58.3%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 1 KTACTAPTAGNY 12
DB 320 KTGAATPTAGGY 331

RESULT 9
REV_SIVCZ
ID_REV_SIVCZ STANDARD; PRT; 124 AA.
AC P17280;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN REV.
OS Chimpanzee immunodeficiency virus (SIV(Cpz)) (CIV).
OC Viruses; Retrodeltaviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Hueb T., Cheynier R., Meyers A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -1- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -1- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52154; CAA36405.1; -.
DR PIR; S09988; VKLJST.
DR HIT; X52154; REVSCPZ.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SQ SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A782 CRC64;

Query Match 55.9%; Score 38; DB 1; Length 124;
Best Local Similarity 58.3%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 2 TAGTAPTAGNYS 13
DB 105 TGTIVPAGNYS 116

RESULT 10

```

RLA0_CHERU STANDARD; PRT; 321 AA.
 ID_RLA0_CHERU
 AC P29764;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 60S acidic ribosomal protein P0 (light-induced 34 kDa protein).
 OS Chenopodium rubrum (Red goosefoot) (Pigweed).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.
 NCBI_TaxID=3560;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kalenhoff R., Richter G.;
 RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT
 CC OF E.COLI PROTEIN L10.
 CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH
 CC DIMERS OF P1 AND P2 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X15206; CAA33276.1; -;
 DR PIR; S21519; RSUBP0.
 DR InterPro; IPR001813; 60S_ribosomal.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR Pfam; PF00428; 60S_ribosomal_L10.
 DR Pfam; PF00466; Ribosomal_L10; 1.
 DR RiboSomal protein; phosphorylation.
 SK SEQUENCE 321 AA; 34351 MW; 3A3333FC86EC0B2 CRC64;
 Query Match 55.9%; Score 38; DB 1; Length 321;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TAGTAPTATG 10
 DB 284 SAGTAPTGG 292

RA Bourisse R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Comerton I.F., Cummings N.J., Daniel R.A.,
 RA Denton F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Gradi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henauf A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaubner-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsreijn G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Melillo R.P., Mizuno M., Moestl D., Nakai S., Nockack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portelle D., Porwollik S., Prescott A.M.,
 RA Priesgen E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT subtilis".
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 1-57 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnard M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
 RA Priesgen E., Santana M., Schneider E., Schweizer J., Verres A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 RT kb region from 325 degrees to 333 degrees".
 RL Mol. Microbiol. 10:371-384(1993).
 RN [4]
 RP SEQUENCE OF 1-9.
 RC STRAIN=168; 1S58;
 RX MEDLINE=9744398; PubMed=9298659;
 RA Antelmann H., Bernhardt J., Schmidt R., Mach H., Voelker U.,
 RA Hecker M.;
 RT "First steps from a two-dimensional protein index towards a response-
 RT regulation map for *Bacillus subtilis*.";
 RL Electrophoresis 18:1451-1463(1997).
 CC -1- FUNCTION: Acts on leucine, isoleucine and valine (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-2-
 CC oxopentanoate + L-glutamate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Valine and isoleucine biosynthesis.
 CC -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z49992; CAA90289.1; -;
 DR EMBL; Z99123; CAB15881.1; -;
 DR EMBL; X73124; CAA51556.1; -;
 DR PIR; S57763; S57763.
 DR HSSP; P00510; IA3G.
 DR Subtilist; BG10546; ywaA.
 DR InterPro; IPR001544; Aminotran_4.
 DR InterPro; IPR005786; B_amino_ttransfer


```

RX MEDLINE=94055391; PubMed=8237108;
RA Sanchez A., Kiley M.P., Holloway B.P., Auperin D.D.;
RT "Sequence analysis of the Ebola virus genome: organization, genetic
RT elements, and comparison with the genome of Marburg virus.";
RL Virus Res. 29:215-240(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire Mayinga;
RL Volchok V.E.;
RU Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-95;
RL MEDLINE=96195018; PubMed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
RT frames and are expressed through transcriptional editing.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
RN
RP PROCESSING.
RL MEDLINE=20072964; PubMed=10603327;
RA Volchok V.A., Kienk H.D., Volchok V.E.;
RT "Delta-peptide is the carboxy-terminal cleavage fragment of the
RT nonstructural small glycoprotein sgp of Ebola virus.";
RL Virology 265:164-171(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE FILOVIRUSES GLYCOPROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U23187; AAC54886.1; -
DR EMBL; U31033; AAA96745.1; -
DR EMBL; AF086833; AAD14584.1; -
DR EMBL; U28077; AAB37094.1; -
DR InterPro; IPR002561; F110_glycop.
DR Pfam; PF01611; F110_glycop; 1.
DR GlycoProtein; signal.
FT CHAIN 1 32 POTENTIAL.
FT SIGNAL 1 32 SMALL/SECRETED GLYCOPROTEIN.
FT CHAIN 33 364 DELTA PEPTIDE.
FT CARBOHYD 33 364
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 364 AA; 41175 MW; 67376A454CE5F362 CRC64;

Query Match 55.9%; Score 38; DB 1; Length 364;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
DB 140 KVSQTGTCACGDF 152

RESULT 15
TCPB_VIBCH STANDARD; PRT; 430 AA.
AC P23476; Q56665;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Toxin coregulated plus biosynthesis protein B (TCP plus
DE biosynthesis protein tcpb).

```

```

GN TCPB OR VC0829.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Classical Inaba Z17561 / Serotype O1, and
RC El Tor H1 / Serotype O1;
RX MEDLINE=96200848; PubMed=8621096;
RA Ogierman M.A., Voss E., Meaney C., Faast R., Attridge S.R.,
RA Manning P.A.;
RT "Comparison of the promoter proximal regions of the toxin-co-regulated
RT tcp gene cluster in classical and El Tor strains of Vibrio cholerae
RT O1.";
RL Gene 170:9-16(1996).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Frazer C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN
RP PRELIMINARY SEQUENCE OF 1-50 FROM N.A.
RX MEDLINE=90152368; PubMed=2576015;
RA Faast R., Ogierman M.A., Stroehner U.H., Manning P.A.;
RT "Nucleotide sequence of the structural gene, tcpA, for a major pilin
RT subunit of Vibrio cholerae.";
RL Gene 85:227-231(1989).
CC -1- FUNCTION: INVOLVED IN TCP PILUS BIOGENESIS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X64098; CAA45456.1; -
DR EMBL; X74730; CAA52746.1; -
DR EMBL; AB004168; AAF93992.1; -
DR EMBL; M33514; -; NOT ANNOTATED_CDS.
DR PIR; JC4720; JC4720.
DR TIGR; VC0829; -.
KM Complete proteome.
FT VARIANT 93 L -> P (IN STRAIN Z17561).
FT VARIANT 202 V -> A (IN STRAIN Z17561).
FT VARIANT 254 T -> S (IN STRAIN Z17561).
FT VARIANT 266 KS -> NA (IN STRAIN Z17561).
SQ SEQUENCE 430 AA; 47118 MW; 3DCD382CSCBDC50F CRC64;

Query Match 55.9%; Score 38; DB 1; Length 430;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGN 11
DB 94 TAGDVPTTGN 103

```

Search completed: February 6, 2004, 11:38:51
Job time : 13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:31 / Search time 35 Seconds

(without alignments)
95.848 Million cell updates/sec

Title: US-09-618-577-28

Perfect score: 68

Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_proteic:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacterioph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	170	2	Q93V20
2	48	70.6	135	2	Q47120
3	47	69.1	134	2	Q47122
4	47	69.1	167	2	Q93G69
5	46	67.6	142	2	Q47124
6	43	63.2	217	1	Q97782
7	42	61.8	82	2	Q8GAD2
8	42	61.8	358	16	Q9KAY0
9	41	60.3	179	10	Q39955
10	41	60.3	181	2	Q9AG87
11	41	60.3	249	5	Q8T306
12	41	60.3	313	10	Q04828
13	41	60.3	560	10	Q94UT1
14	41	60.3	573	5	Q8WS24
15	41	60.3	672	11	Q8CG10
16	41	60.3	685	11	Q8C1S1

17	41	60.3	795	11	Q9DBY0
18	41	60.3	965	5	Q9VAM5
19	41	60.3	1403	5	Q9NHM6
20	41	60.3	1403	5	Q8IMM4
21	40	58.8	346	10	Q82525
22	40	58.8	362	10	Q9FMG1
23	40	58.8	469	12	Q8B198
24	40	58.8	469	12	Q8B197
25	40	58.8	506	11	Q8K383
26	40	58.8	787	10	Q9FCG1
27	40	58.8	792	5	Q23115
28	40	58.8	956	10	Q8RMH3
29	40	58.8	1275	4	Q9UQ36
30	40	58.8	1783	4	Q15038
31	40	58.8	1791	4	Q60382
32	40	58.8	2607	11	Q8BRT8
33	40	58.8	2752	4	Q9UQ35
34	39	57.4	144	9	Q9G0F9
35	39	57.4	234	2	Q8GF82
36	39	57.4	256	10	Q24568
37	39	57.4	285	10	Q8H367
38	39	57.4	426	10	Q8S5V5
39	39	57.4	724	5	Q9GT88
40	39	57.4	890	10	Q8W5R6
41	39	57.4	909	10	Q9X103
42	39	57.4	928	16	Q8PEU8
43	39	57.4	1216	11	Q8BUP1
44	38	56.6	241	12	Q89247
45	38	55.9	67	2	Q9X6L7

ALIGNMENTS

RESULT 1

Q93V20 ID Q93V20 PRELIMINARY; PRT; 170 AA.

AC Q93V20;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Colonization factor antigen 1.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94207144; PubMed=8155840;

RA Zhang Z., Li S., Huang C.;

RT "Sequence analysis of the colonization factor antigen 1 gene of ETEC RT and observation of CPA/1 recombinant clone with electron microscopy.";

RL Chin. J. Biotechnol. 9:57-61 (1993).

DR EMBL; S73191; AAB30543.1; -

DR Pfam; PF04449; Fimbrin CSI; 1.

SQ SEQUENCE 170 AA; 17433 MW; 894347E2P43S5B4 CRC64;

Query Match 100.0%; Score 68; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
DB 147 KTAGTAPTAGNYS 159

RESULT 2

Q47120 ID Q47120 PRELIMINARY; PRT; 135 AA.

AC Q47120;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

```

DE CsaA protein (Fragment).
GN CSAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E20738A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa14 fimbriae is duplicated in the CS14
RT fimbrial operon."
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97495; CAA6126.1; -.
FT NON_TER 1 135
SQ SEQUENCE 135 AA; 14277 MW; 88964DB09C944B6F CRC64;

Query Match
Best Local Similarity 70.6%; Score 48; DB 2; Length 135;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12
DB 113 TGTATPEAGNY 123

RESULT 3
Q47122 PRELIMINARY; PRT; 134 AA.
AC Q47122;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CsaA protein (Fragment).
GN CSFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9b1373;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa14 fimbriae is duplicated in the CS14
RT fimbrial operon."
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97493; CAA6124.1; -.
FT NON_TER 1 134
SQ SEQUENCE 134 AA; 13916 MW; 3EEFFDC5861396A4 CRC64;

Query Match
Best Local Similarity 69.1%; Score 47; DB 2; Length 134;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNYS 13
DB 112 TTAQAPTAGNYS 123

RESULT 4
Q93669 PRELIMINARY; PRT; 167 AA.
AC Q93669;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CS4 major fimbriae subunit CsaB.
GN CSAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

```

```

OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1181A;
RA Altboum Z.D., Levine M.M., Galen J.E., Barry E.M.;
RT "Isolation and characterization of EPEC CS4 fimbriae encoding genes,
RT and their expression in Shigella flexneri 2a guaba strain CVD 1204."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF296132; AAK97135.1; -.
FT Pfam; PF04449; Fimbril_CS1; 1.
SQ SEQUENCE 167 AA; 17344 MW; 94C7822A7C23A5A CRC64;

Query Match
Best Local Similarity 69.1%; Score 47; DB 2; Length 167;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNYS 13
DB 145 TTAQAPTAGNYS 156

RESULT 5
Q47124 PRELIMINARY; PRT; 142 AA.
AC Q47124;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CsaA2 protein (Fragment).
GN CSUA2.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E7476A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa14 fimbriae is duplicated in the CS14
RT fimbrial operon."
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97492; CAA6123.1; -.
DR InterPro; IPR00719; Prot_Kinase.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
FT NON_TER 1 142
SQ SEQUENCE 142 AA; 14498 MW; 932BF1A7989A4E7D CRC64;

Query Match
Best Local Similarity 67.6%; Score 46; DB 2; Length 142;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12
DB 113 TSGTAPSAKY 123

RESULT 6
Q977R2 PRELIMINARY; PRT; 217 AA.
AC Q977R2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NAD(P)H-flavin oxidoreductase.
OS unclutured crenarchaeote 487.
OC Archaea; Crenarchaeota; environmental samples;
OC marine archaeal group 1.
OX NCBI_TaxID=44557;
RN [1]
RP SEQUENCE FROM N.A.
RA Beja O., Koonin E.V., Aravind L., Taylor L.T., Seitz H., Stein J.L.,
RA Bensen D.C., Feldman R.A., Swanson R.V., Delong E.F.;

```


RT "Comparative genomic analysis of coexisting archaeal genetic variants
 in an Antarctic marine microbial assemblage.";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40338; AK66808.1; -;
 DR InterPro; IPR000415; Nitroreductase.
 DR Pfam; PF00881; Nitroreductase; 1.
 SO SEQUENCE 217 AA; 24624 MW; E22C83BD4957E67 CRC64;
 Query Match 63.2%; Score 43; DB 1; Length 217;
 Best Local Similarity 80.0%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 AGTAPTAGNT 12
 Db 78 ADTAPTAGNF 87
 RESULT 7
 ID O8GAD2 PRELIMINARY; PRT; 82 AA.
 AC O8GAD2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative transposase (Fragment).
 OS Arthrobacter nicotinovorus.
 OG Plasmid pAO1.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=29320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95115562; PubMed=7815950;
 RA Grether-Beck S., Iglol G.L., Pust S., Schiltz E., Decker K.,
 Brandach R.;
 RT "Structural analysis and molybdenum-dependent expression of the pAO1-
 encoded nicotinic dehydrogenase genes of Arthrobacter nicotinovorus.";
 RL Mol. Microbiol. 13:929-936(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96172783; PubMed=8588735;
 RA Menendez C., Iglol G., Heminger H., Brandach R.;
 RT "A pAO1-encoded molybdopterin cofactor gene (moaA) of Arthrobacter
 nicotinovorus: characterization and site-directed mutagenesis of the
 encoded protein.";
 RL Arch. Microbiol. 164:142-151(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97230479; PubMed=9073580;
 RA Menendez C., Iglol G.L., Brandach R.;
 RT "Is1473, a putative insertion sequence identified in the plasmid pAO1
 from Arthrobacter nicotinovorus: isolation, characterisation and
 distribution among Arthrobacter species.";
 RL Plasmid 37:35-41(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98088982; PubMed=9428706;
 RA Menendez C., Otto A., Iglol G., Nick P., Brandach R., Schubach B.,
 Botcher B., Brandach R.;
 RT "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a
 bacterial plasmid. Characterization of MoaA as a filament-forming
 protein with adenosinetriphosphatase activity.";
 RL Eur. J. Biochem. 250:524-531(1997).
 [5]
 RP SEQUENCE FROM N.A.
 RX Schenk S., Hoelz S., Kraus B., Decker K.;
 RT "Gene structure and properties of enzymes of the plasmid-encoded
 RT nicotine catabolism of Arthrobacter nicotinovorus.";
 RL J. Mol. Biol. 284:1323-1339(1999).
 [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21405725; PubMed=11514508;
 RA Batsch D., Sandu C., Brandach R., Iglol G.L.;

RT "A gene cluster on pAO1 of Arthrobacter nicotinovorus involved in the
 RT degradation of the plant alkaloid nicotine: cloning, purification and
 RT characterization of 2,6-dihydroxypyridine 3-hydroxylase.";
 RL J. Bacteriol. 183:5262-5267(2001).
 [7]
 RP SEQUENCE FROM N.A.
 RA Iglol G.L., Brandach R.;
 RT "Sequence of the 165 kb Catabolic Plasmid pAO1 from Arthrobacter
 RT nicotinovorus and Identification of a pAO1-dependent Nicotine Uptake
 RT System.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ507836; CAD47999.1; -;
 KW Plasmid.
 FT NON_TER 1
 FT NON_TER 82
 SO SEQUENCE 82 AA; 8718 MW; 16317803035C8140 CRC64;
 Query Match 61.8%; Score 42; DB 2; Length 82;
 Best Local Similarity 88.9%; Pred. No. 8.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TAGTAPTAG 10
 Db 44 SAGTAPTAG 52
 RESULT 8
 ID O9KAY0 PRELIMINARY; PRT; 358 AA.
 AC O9KAY0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)
 DE Branched-chain amino acid aminotransferase (BC 2.6.1.42).
 GN BCAT OR BH2156.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=8665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeni N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001514; BAB05875.1; -;
 DR HSSP; P00510; 1A3G.
 DR InterPro; IPR001544; Aminotran_4.
 DR InterPro; IPR005786; B_amino_transit.
 DR Pfam; PF01063; aminotran_4; 1.
 DR ProDom; PD001961; Aminotran_4; 1.
 DR TIGRFAMs; TIGR01123; lIve II; 1.
 DR PROSITE; PS00770; AA TRANSFER CLASS 4; 1.
 KW Transferase; Aminotransferase; Complete proteome.
 SO SEQUENCE 358 AA; 40658 MW; B25FFB62BECF9001 CRC64;
 Query Match 61.8%; Score 42; DB 16; Length 358;
 Best Local Similarity 80.0%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GTAPTAGNTS 13
 Db 194 GTAPTAGNTS 203
 RESULT 9
 ID Q39995 PRELIMINARY; PRT; 179 AA.
 AC Q39995;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE 30 kDa pollen allergen (Fragment).
 GN GIX1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Hordeum.
 OX NCB1_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Astwood J.D.;
 RT "Developmental and molecular characterization of pollen allergen
 cognates in barley.";
 RL Thesis (1993), Plant Science, University of Manitoba.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Astwood J.D., Hill R.D.;
 RT "Identification and expression of a high pI protein gene family in
 barley pollen.";
 RL Plant Physiol. 102:10-10(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Astwood J.D.;
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U06640; AAA16702.1; -.
 DR InterPro; IPR001778; POA_allergenc.
 DR InterPro; IPR002914; POA_allergenn.
 DR Pfam; PF01620; Pollen_allerg_2; 1.
 DR PRINTS; PR00833; POAALLERGEN.
 FT NON TER 1
 SQ SEQUENCE 179 AA; 18371 MW; 82D968F4F6EAECE CRC64;

Query Match 60.3%; Score 41; DB 10; Length 179;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGTAPTAGNY 12
 DB 168 AGAATAGNY 177

RESULT 10
 OYAG87
 ID 09AG87 PRELIMINARY; PRT; 181 AA.
 AC 09AG87;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CsuA.
 GN CsuA.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrilo.
 OX NCB1_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BB22;
 RA McCarter L.L., Welsh C., Boles B.;
 RT "The *csu* locus of *Vibrio parahaemolyticus*.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF339087; AAK37520.1; -.
 SQ SEQUENCE 181 AA; 18972 MW; 53CCEBBA3918CD09 CRC64;

Query Match 60.3%; Score 41; DB 2; Length 181;
 Best Local Similarity 61.5%; Pred. No. 28;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGNYS 13
 DB 160 KAYGTSTAGSYS 172

RESULT 11
 ID 08T306 PRELIMINARY; PRT; 249 AA.
 AC 08T306;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Helix-loop-helix transcription factor.
 GN HAIRY.
 OS Tribolium castaneum (Red flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
 OC Tenebrionidae; Tribolium.
 OX NCB1_TaxID=7070;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eckert C., Wolf C., Wimmer E., Tautz D.;
 RT "Functional analysis of the regulatory region of the pair-rule gene
 hairy in *Tribolium* suggests regulatory divergence inspite of conserved
 expression.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 TRANSCRIPTION FACTORS.
 DR EMBL; AJ457831; CAD29886.1; -.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR003650; Orange.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00511; ORANGE; 1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR PROSITE; PS50888; HLH_2; 1.
 SQ SEQUENCE 249 AA; 27252 MW; 364BB299EBBFA429B CRC64;

Query Match 60.3%; Score 41; DB 5; Length 249;
 Best Local Similarity 61.5%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGNYS 13
 DB 205 RTASTASSASNYS 217

RESULT 12
 ID 004828 PRELIMINARY; PRT; 313 AA.
 AC 004828;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Pollen allergen precursor.
 GN HORV9.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Hordeum.
 OX NCB1_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97136690; PubMed=8982067;
 RA Astwood J.D., Hill R.D.;
 RT "Cloning and expression pattern of *Hor v 9*, the group 9 pollen
 isoallergen from barley.";
 RL Gene 182:53-62(1996).
 DR EMBL; U57845; AAB41585.1; -.
 DR InterPro; IPR001778; POA_allergenc.
 DR InterPro; IPR002914; POA_allergenn.
 DR Pfam; PF01620; Pollen_allerg_2; 1.
 DR PRINTS; PR00833; POAALLERGEN.
 KW SIGNAL.
 FT CHAIN 28 313 POTENTIAL.
 FT SIGNAL 28 313 POLLEN ALLERGEN.
 SQ SEQUENCE 313 AA; 33147 MW; D6D174B5D3090005 CRC64;

Query Match 60.3%; Score 41; DB 10; Length 313;
 Best Local Similarity 80.0%; Pred. No. 50;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGTAPTAGNY 12
 DB 302 AGAATAGNY 311

RESULT 13

ID 094JTL PRELIMINARY; PRT; 560 AA.
 AC 094JTL;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE ATGg42740/MJb21_12 (EC 5.3.1.9) (Glucose-6-phosphate isomerase) (GPI)
 DE (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase)
 DE (PHI).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowers L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shin P., Banh J.,
 RA Bowers L., Carninci P., Chang B., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE = D-FRUCTOSE 6-PHOSPHATE.
 CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
 DR EMBL; AF372970; AAK50107.1; -;
 DR EMBL; AY093962; AAM16223.1; -;
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; PGI; 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Glucosogenesis; Glycolysis; Isomerase.
 SQ SEQUENCE 560 AA; 61657 MW; 0ACC69EB82A534CD CRC64;

Query Match 60.3%; Score 41; DB 10; Length 560;
 Best Local Similarity 61.5%; Pred. No. 93;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGNY 13
 DB 531 RTGCTAPGPNYS 543

RESULT 14

ID 08MSZ4 PRELIMINARY; PRT; 573 AA.
 AC 08MSZ4;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE GW07509P.
 GN LARP OR CG14066.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommler B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceollier S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY118468; AAM49837.1; -;
 DR FLYBase; FBgn040108; larp.
 DR InterPro; IPR006607; DDF_DM15.
 DR SMART; SM00684; DM15; 3.
 SQ SEQUENCE 573 AA; 64261 MW; E9637D6759D9BFF CRC64;

Query Match 60.3%; Score 41; DB 5; Length 573;
 Best Local Similarity 63.6%; Pred. No. 95;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAGNY 12
 DB 205 SAGTSPTASSY 215

RESULT 15
 ID 08CG10 PRELIMINARY; PRT; 672 AA.
 AC 08CG10;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Fork head-related protein like A.
 GN MFKHLA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Daigo Y., Takayama I., Fujino M.A.;
 RT "Isolation and characterization of novel human and mouse genes, which
 RT are expressed in the digestive tract";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB052766; BAC53799.1; -;
 SQ SEQUENCE 672 AA; 72758 MW; 8B89F59EF85FC768 CRC64;

Query Match 60.3%; Score 41; DB 11; Length 672;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAG 10
 DB 35 TAGTAPAG 43

Search completed: February 6, 2004, 11:40:13
 Job time : 37 secs

THIS PAGE BLANK (USPTO)

Refine Search

Search Results -

Terms	Documents
5705197.pn.	1

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L7

Search History

DATE: Friday, February 06, 2004 [Printable Copy](#) [Create Case](#)

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=OR

<u>L7</u>	5705197.pn.	1	<u>L7</u>
<u>L6</u>	5693343.pn.	1	<u>L6</u>
<u>L5</u>	L4 and l3	7	<u>L5</u>
<u>L4</u>	CFA/I	48	<u>L4</u>
<u>L3</u>	biocompatible and L2	3595	<u>L3</u>
<u>L2</u>	L1 and biodegradable microphere	12076	<u>L2</u>
<u>L1</u>	burst-free programmable sustained release	642821	<u>L1</u>

END OF SEARCH HISTORY

THIS PAGE BLANK (USPTO)

Refine Search

Search Results -

Terms	Documents
L4 and L3	7

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L5

Refine Search

Recall Text

Clear

Interrupt

Search History

DATE: Friday, February 06, 2004 [Printable Copy](#) [Create Case](#)

Set Name Query

side by side

DB=USPT; PLUR=YES; OP=OR

Hit Count Set Name

result set

<u>L5</u>	L4 and l3	7	<u>L5</u>
<u>L4</u>	CFA/I	48	<u>L4</u>
<u>L3</u>	biocompatible and L2	3595	<u>L3</u>
<u>L2</u>	L1 and biodegradable microsphere	12076	<u>L2</u>
<u>L1</u>	burst-free programmable sustained release	642821	<u>L1</u>

END OF SEARCH HISTORY

THIS PAGE BLANK (USPTO)

Hit List

[Clear](#)[Generate Collection](#)[Print](#)[Fwd Refs](#)[Bkwd Refs](#)[Generate OACS](#)

Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 6531156 B1

L5: Entry 1 of 7

File: USPT

Mar 11, 2003

US-PAT-NO: 6531156

DOCUMENT-IDENTIFIER: US 6531156 B1

TITLE: Aqueous solven encapsulation method, apparatus and microcapsules

DATE-ISSUED: March 11, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Clark; Fred M.	Philadelphia	PA		
Offit; Paul A.	Bala Cynwyd	PA		
Speaker; Tully J.	Philadelphia	PA		

US-CL-CURRENT: [424/489](#); [426/490](#), [426/492](#), [426/496](#), [426/497](#), [426/499](#), [426/500](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw. D
----------------------	-----------------------	--------------------------	-----------------------	------------------------	--------------------------------	----------------------	---------------------------	---------------------------	-----------------------------	------------------------	---------------------	-------------------------

☐ 2. Document ID: US 6528097 B1

L5: Entry 2 of 7

File: USPT

Mar 4, 2003

US-PAT-NO: 6528097

DOCUMENT-IDENTIFIER: US 6528097 B1

TITLE: Sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheres

DATE-ISSUED: March 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vaughn; William M.	Silver Spring	MD		
Van Hamont; John E.	Ft. Meade	MD		
Setterstrom; Jean A.	Alpharetta	GA		

US-CL-CURRENT: [424/501](#); [424/422](#), [514/570](#)

THIS PAGE BLANK (USPTO)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	----------

☐ 3. Document ID: US 6447796 B1

L5: Entry 3 of 7

File: USPT

Sep 10, 2002

US-PAT-NO: 6447796

DOCUMENT-IDENTIFIER: US 6447796 B1

**** See image for Certificate of Correction ****TITLE: Sustained release hydrophobic bioactive PLGA microspheres

DATE-ISSUED: September 10, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vook; Noelle Christine	Schaumburg	IL		
Jacob; Elliott	Silver Spring	MD		
Setterstrom; Jean A.	Alpharetta	GA		
van Hamont; John	West Point	NY		
Vaughan; William	Silver Spring	MD		
Duong; Ha	Montclair	CA		

US-CL-CURRENT: 424/422; 424/426, 424/457, 424/468

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	----------

☐ 4. Document ID: US 6410056 B1

L5: Entry 4 of 7

File: USPT

Jun 25, 2002

US-PAT-NO: 6410056

DOCUMENT-IDENTIFIER: US 6410056 B1

TITLE: Chemotherapeutic treatment of bacterial infections with an antibiotic encapsulated within a biodegradable polymeric matrix

DATE-ISSUED: June 25, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Setterstrom; Jean A.	Silver Spring	MD		
Jacob; Elliot	Silver Spring	MD		
Tice; Thomas R.	Birmingham	AL		

US-CL-CURRENT: 424/501; 424/502, 428/402.24, 514/772.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	----------

THIS PAGE BLANK (USPTO)

☐ 5. Document ID: US 6309669 B1

L5: Entry 5 of 7

File: USPT

Oct 30, 2001

US-PAT-NO: 6309669

DOCUMENT-IDENTIFIER: US 6309669 B1

TITLE: Therapeutic treatment and prevention of infections with a bioactive materials encapsulated within a biodegradable-biocompatible polymeric matrix

DATE-ISSUED: October 30, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Setterstrom; Jean A.	Alpharetta	GA		
Van Hamont; John E.	Fort Meade	MD		
Reid; Robert H.	McComas	CT		
Jacob; Elliot	Silver Spring	MD		
Jeyanthi; Ramasubbu	Columbia	MD		
Boedeker; Edgar C.	Chevy Chase	MD		
McQueen; Charles E.	Olney	MD		
Jarboe; Daniel L.	Silver Spring	MD		
Cassels; Frederick	Ellicott City	MD		
Brown; William	Denver	CO		
Thies; Curt	Ballwin	MO		
Tice; Thomas R.	Birmingham	AL		
Roberts; F. Donald	Dover	MA		
Friden; Phil	Beford	MA		

US-CL-CURRENT: 424/486, 424/422, 424/423, 424/424, 424/425, 424/484

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	----------

☐ 6. Document ID: US 6217911 B1

L5: Entry 6 of 7

File: USPT

Apr 17, 2001

US-PAT-NO: 6217911

DOCUMENT-IDENTIFIER: US 6217911 B1

**** See image for Certificate of Correction ****

TITLE: sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheres

DATE-ISSUED: April 17, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vaughn; William M.	Silver Spring	MD		

THIS PAGE BLANK (USPTO)

Van Hamont; John E. Ft. Meade MD
Setterstrom; Jean A. Alpharetta GA

US-CL-CURRENT: 424/501; 424/422, 514/570

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	----------

☐ 7. Document ID: US 5417986 A

L5: Entry 7 of 7

File: USPT

May 23, 1995

US-PAT-NO: 5417986

DOCUMENT-IDENTIFIER: US 5417986 A

TITLE: Vaccines against diseases caused by enteropathogenic organisms using antigens encapsulated within biodegradable-biocompatible microspheres

DATE-ISSUED: May 23, 1995

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Reid; Robert H.	Kensington	MD		
Boedeker; Edgar C.	Chevy Chase	MD		
van Hamont; John E.	Shape			BE
Setterstrom; Jean A.	Takoma Park	MD		

US-CL-CURRENT: 424/499; 424/422, 424/426, 424/433, 424/444, 424/455, 424/470,
424/486, 424/488, 424/489, 424/491

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	----------

Clear

Generate Collection

Print

Fwd Refs

Bkwd Refs

Generate OACS

Terms

Documents

L4 and L3

7

Display Format: CIT

Change Format

[Previous Page](#)

[Next Page](#)

[Go to Doc#](#)

THIS PAGE BLANK (USPTO)

[First Hit](#) [Fwd Refs](#)

Generate Collection

Print

L5: Entry 2 of 7

File: USPT

Mar 4, 2003

DOCUMENT-IDENTIFIER: US 6528097 B1

TITLE: Sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheresAbstract Text (1):

A controlled release microcapsule pharmaceutical formulation for burst-free, sustained, programmable release of a non-steroidal, antiinflammatory drug over a duration from 24 hours to 2 months, comprising: a non-steroidal, antiinflammatory drug and a blend of biocompatible, biodegradable poly (lactide/glycolide).

Brief Summary Text (2):

This invention relates to providing novel pharmaceutical compositions for local delivery and sustained release of non-steroidal, anti-inflammatory drugs (NSAIDS) from biocompatible, biodegradable poly(DL-lactide-co-glycolide) (PLGA) microspheres. The resulting product is applied locally into soft tissues surrounding a surgical incision or traumatic wound site where it will locally sustain release of the NSAID.

Brief Summary Text (3):

The invention also relates to providing novel pharmaceutical compositions for local delivery and sustained release of lidocaine PLGA microspheres.

Brief Summary Text (5):

Non-steroidal anti-inflammatory drugs (NSAIDS) have been effective in reducing inflammation and inducing analgesia; however, the conventional oral dosage forms of these drugs characteristically have short half-lives and irritate the gastrointestinal mucosa. Further, currently available slow release oral dosage forms, such as Biovail (enteric coated, double-layer tablets which release the drug for 12-24 hours) still result in inefficient systemic delivery of the drug and potential gastrointestinal irritation.

Brief Summary Text (6):

Therefore, currently available slow release oral dosage forms of NSAIDs induces systemic effects and the drug is not efficiently used at the site of inflammation.

Brief Summary Text (7):

Further, in the currently available slow release oral dosage forms of NSAIDs, fillers or additives are needed in order to accelerate or retard drug release.

Brief Summary Text (9):

Several publications and patents are available for sustained release of active agents from biodegradable polymers, particularly, poly(lactide/glycolides) (PLGA). Prior usages of PLGA for controlled release of polypeptides have involved the use of molar ratios of lactide/glycolide (L/G) of 75/25 to 100/0 for molecular weights >20,000. Further, prior art preparations of PLGA utilized fillers or additives in the inner aqueous layer to improve stability and encapsulation efficiency and/or to increase the viscosity of the aqueous layer, thereby modulating polymer hydrolysis and the biologically active agent or polypeptide release.

Brief Summary Text (10):

THIS PAGE BLANK (USPTO)

In addition, the prior art use of PLGA copolymers were end-capped, in that the terminal carboxyl end groups were blocked. In these end-capped co-polymers, the microcapsule preparations exhibited a low to moderate burst release of .about.10-14% of the entrapped polypeptide in the first 24 hours after placement in an aqueous physiological environment. In part, these characteristics are due to the use of fillers in the inner aqueous phase. Further, a 1-month release of polypeptide is known with the use of a 75/25 co-polymer of PLGA of Mw <20,000.

Brief Summary Text (11):

Investigations in controlled release research has been proceeding especially to obtain a 1-2 month delivery system for biologically active agents or polypeptides using poly(lactide/glycolide) polymers. However, most of these systems have one or more of the following problems: poor encapsulation efficiency and large 'burst release' followed by an intermediate 'no release' or 'lag phase' until the polymer degrades. In general, release from these polymers occur over a period from about 4 weeks to about several months. In addition, in order to achieve this release a 50/50 co-polymer of Mw>30,000 or a 75/25 co-polymer of Mw>10,000 are employed which often results in residual polymer remaining at the site of administration long after the release of active core.

Brief Summary Text (13):

This invention provides novel pharmaceutical compositions for local delivery and sustained release of non-steroidal, anti-inflammatory drugs (NSAIDs) from biocompatible, biodegradable poly(DL-lactide-co-glycolide) (PLGA) microspheres. The resulting product is applied locally into soft tissues surrounding a surgical incision or traumatic wound site where it will locally sustain release the NSAID. In the context of this invention, ketoprofen, is preferred. Ketoprofen is an important non-steroidal anti-inflammatory drug, and is formulated into a drug delivery system that releases the drug in an aqueous solution or soft tissue for 7-60 days, depending upon its formulation.

Brief Summary Text (14):

The invention also provides novel pharmaceutical compositions for local delivery and sustained release of lidocaine PLGA microspheres.

Brief Summary Text (15):

One object of the invention is to provide biodegradable PLGA microspheres for sustained delivery of NSAIDs.

Brief Summary Text (16):

Another object of the invention is to provide sustained, local delivery of NSAIDs, for durations greater than 24 hours and for up to 2 months from a single dose.

Brief Summary Text (19):

A yet further object of the invention is to provide oral dosage forms incorporating compositions of NSAID-loaded microspheres of this invention to deliver the microspheres to the gastrointestinal lumen where they can be adsorbed within the epithelium and sustain release their contents systemically.

Brief Summary Text (21):

A further object yet still is to provide sustained released lidocaine PLGA microspheres for the treatment of dental pain.

Brief Summary Text (24):

In the solvent evaporation process, the NSAID and PLGA were dissolved in a volatile organic solvent, preferably methylene chloride, and dispersed in an aqueous phase containing an emulsion stabilizer. Evaporation of the organic phase gave NSAID-loaded microspheres. Depending on processing parameters, the microspheres released the NSAID for a duration of 2 weeks to 2 months with minimal burst release.

THIS PAGE BLANK (USPTO)

Drawing Description Text (4):

FIG. 3 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation. The release profiles are biphasic with a slower release in the first week followed by a more rapid release during the second week.

Drawing Description Text (5):

FIG. 4 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation with increased initial polymer concentrations. A zero-order release of ketoprofen over 33 days is obtained. WV51a was prepared at reduced PLGA concentrations.

Drawing Description Text (6):

FIG. 5 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation at 40.degree. C. demonstrating a zero-order release of 40-60% of the loaded ketoprofen followed by a terminal burst release of the remaining drug. WV29 was prepared at 20.degree. C.

Drawing Description Text (7):

FIG. 6 shows ketoprofen release profiles from PLGA microspheres prepared by solvent extraction demonstrating 7-10 day release.

Drawing Description Text (10):

FIG. 9 shows release profiles of lidocaine-PLGA microspheres prepared by solvent evaporation.

Drawing Description Text (11):

FIG. 10 shows release profiles of lidocaine hydrochloride PLGA formulations prepared by solvent extraction.

Detailed Description Text (2):

This invention relates to the design of biocompatible and biodegradable microspheres for novel, sustained release of non-steroidal, anti-inflammatory drugs, including ketoprofen, over a period of up to 60 days in an aqueous physiological environment with little or no burst release.

Detailed Description Text (3):

Unlike currently available release systems which rely on the use of filler/additives such as gelatin, albumin, dextran, pectin, polyvinyl pyrrolidone, polyethylene glycol, sugars, etc., and are still prone to low encapsulation efficiencies and "burst effects", this invention achieves high encapsulation efficiency and 'burst-free' release without the use of any additive. In this invention, 'burst-free', programmable sustained release is achieved.

Detailed Description Text (5):

Additionally, two forms of the biocompatible, biodegradable poly(DL-/lactide-shield-glycolide) can be employed, one being the more hydrophobic end-capped polymer with the terminal residues functionalized as esters, and the other being the more hydrophilic uncapped polymer with the terminal residues existing as carboxylic acids.

Detailed Description Text (8):

Ketoprofen and PLGA were dissolved in methylene chloride, and dispersed in an aqueous phase containing an emulsion stabilizer. Evaporation of the organic phase gave ketoprofen-loaded microspheres, as is shown in FIGS. 1, 3, 4, and 5. The microspheres release ketoprofen for a duration of two weeks to two months with minimal burst release as can be seen from the foregoing referred to figures.

Detailed Description Text (11):

In the solvent extraction process, ketoprofen and PLGA were dissolved in acetonitrile, which is a polar organic solvent, and the mixture of ketoprofen, PLGA

THIS PAGE BLANK (USPTO)

and acetonitrile is then dispersed in a mineral oil; however, any non-polar organic phase other than mineral oil will suffice in the context of the invention, even though mineral oil is preferred. The emulsion produced is then poured into a hydrocarbon solvent, preferably heptane. As the mineral oil phase was extracted into the heptane, microspheres of PLGA and ketoprofen are formed. The microspheres produced release ketoprofen for seven to ten days displaying near zero-order kinetics. Microspheres produced using this solvent extraction process are shown in FIGS. 2 and 6.

Detailed Description Text (13):

The NSAIDs are prescribed for arthritic conditions to reduce pain and delay debilitating inflammation, and a single, localized dose into joints lasting 2-3 months is very advantageous. Further, the microspheres of the invention are suitable for incorporation into a number of delivery vehicles to provide sustained release of a NSAID-loaded for many other applications for the treatment of mild pain and inflammation.

Detailed Description Text (22):

Ketoprofen release profiles were determined in vitro for the PLGA microspheres. Microspheres were suspended in 1 ml phosphate buffer solution maintained at 37.+- .1.degree. C. in a shaker bath. The buffer was removed and refreshed over time. The ketoprofen concentration was determined by HPLC.

Detailed Description Text (27):

Characteristically, ketoprofen-PLGA microspheres prepared by solvent evaporation slowly released 25-35% of their contents during the first week. This release was followed by an accelerated release of the remaining drug during the next 7-10 days. After 50 days, the hydrated microspheres had not significantly degraded.

Detailed Description Text (28):

Factors contributing to the lag time before significant release was observed include the high molecular weight (70k-100k g/mol) and hydrophobic nature of the PLGA resulting in slow hydration of the microspheres. Also, SEM analysis showed product spheres to be relatively free of defects reducing the possibility of a burst release. Similar profiles of an accelerated release beginning at 7-10 days were observed for lidocaine-PLGA formulations with the same polymer molecular weight. Release is independent of the core loading for this narrow range of 1.5-13.5%.

Detailed Description Text (29):

Heated solvent evaporation formulations (core loads: 7.6, 7.3%) demonstrate zero-order, more sustained release. At 30 days, only 30% of the ketoprofen is estimated to be released.

Detailed Description Text (30):

Ketoprofen-PLGA formulations prepared by solvent extraction show a steady and complete release of ketoprofen in 7-10 days (FIG. 6). The increased surface area of these smaller diameter microspheres contribute to the observed release. The near-linear release indicates the drug is evenly distributed throughout the PLGA matrix. Such release characteristics are highly beneficial for use as anti-inflammatory pulp-capping materials.

Detailed Description Text (31):

Ketoprofen and PLGA combined to form a miscible and homogeneous solid matrix of drug microspheres. This result affords steady and sustained ketoprofen release vehicles for potential use for localized inflammation. In relation to the treatment of pulpitis, plastic chambers are being used to model interactions between ketoprofen and dentin, inflamed pulpal tissue, and common pulp capping dressings such as calcium hydroxide.

THIS PAGE BLANK (USPTO)

Detailed Description Text (35):

This study proposes to evaluate the safety, analgesic efficacy, and tissue response of locally applied ketoprofen [a non steroidal anti-inflammatory drug (NSAID)] that is encapsulated within small microspheres of the biodegradable polymer poly DL (lactide-co-glycolide). The response to encapsulated ketoprofen will be compared to a long-acting local anesthetic such as tetracaine, lidocaine, etidocaine, carbocaine, xylocaine, marcaine, nesacaine and etiod. Both drug formulations will be instilled into post-extraction sites immediately upon extraction of the tooth, but prior to the onset of pain (patients will be under the influence of local anesthetic during the extraction procedure). Subjects (n=84) will have two mandibular impacted third molars removed and be randomly allocated to receive one of six possible treatments placed into the resulting sockets: 0 mg (placebo formation), 3.125 mg, 6.25 mg, or 25 mg ketoprofen, or 50 mg bupivacaine. Each patient in these six groups (n=12/group) will also receive an oral placebo capsule. The seventh group of the subjects will receive a placebo applied at the extraction sites and 25 mg of ketoprofen orally. Subjects will remain at the clinic for six hours following drug administration. Every 30 minutes the offset of mandibular anesthesia, postoperative pain intensity, side effects, and recurrence of bleeding will be monitored. Demonstration of a dose-response relationship for ketoprofen at doses lower than needed for analgesia following oral administration will provide the basis for a follow-up study in which an optimal dose of ketoprofen will be combined with bupivacaine.

Detailed Description Text (38):

The introduction of NSAIDs for the management of acute and chronic pain has resulted in improved analgesia and decreased side effects; however, there remain drawbacks such as a relatively slow therapeutic onset when taken orally, a ceiling of efficacy, and side effects with chronic use (NSAIDs will produce small amounts of GI bleeding at therapeutic doses which can result in ulcers with chronic use in approximately 25% of individuals). An alternative to administering high systematic doses for greater efficacy and a likely way to eliminate side effects is to sustain release NSAIDs or other drugs at the site of injury thereby achieving high local concentrations. This proposed study will evaluate the local administration of an NSAID into tooth extraction sites to determine if such a localized effect can be demonstrated. If demonstrated, it will provide a basis for evaluating the peripheral effects of other putative inhibitors and antagonists of the inflammatory process using this or a similar approach. Despite advantages of NSAIDs for pain management, a therapeutic void remains for the management of pain with a drug modality that has rapid onset by non-parenteral routes of administration and greater efficacy than can be achieved with oral NSAIDs.

Detailed Description Text (55):

Adverse Effects of Microencapsulated Ketoprofen: The adverse effects attributed to orally administered ketoprofen are similar to those associated with other NSAIDs: GI irritation and upset, and impairment of renal function with chronic administration. Administration of ketoprofen (the free drug form) into extraction sites in two previous studies done at NIDR was not associated with any detectable increase in localized adverse effects such as alveolar osteitis or infection in 50 subjects.^{sup.1,2} It is recognized that the administration of an NSAID into the extraction site prior to blood clot formation may result in an increase in postoperative bleeding due to the temporary inhibitory effects of NSAIDs on platelet aggregation. Direct administration of 30 mg of aspirin into the extraction sites following oral surgery has been reported not to produce any increase in bleeding episodes or alveolar osteitis.^{sup.3} Subjects will be observed for any signs of bleeding during the six hour observation period and prior to dismissal from the clinic. The presense of the encapsulation excipient DL (lactide-co-glycolide) may possibly be associated with an increase in the infection rate; however, since it is the same polymer used in biodegradable suture materials (which have a very low infection rate in other surgeries), it is considered unlikely.

THIS PAGE BLANK (USPTO)

Detailed Description Text (71):

Lidocaine release profiles were determined in vitro for the PLGA microspheres. Microspheres were suspended in a phosphate buffer solution maintained at 37.+- .1.degree. C. in a shaker bath, and aliquots were taken during the release period. The lidocaine concentration was determined by HPLC as stated above.

Detailed Description Text (74):

Cumulative release profiles for solvent evaporation and solvent extraction formulations are shown in FIGS. 9 and 10, respectively. In FIG. 9, lidocaine-PLGA microspheres prepared by solvent evaporation slowly released 5-15% of their contents during the first week. This release was followed by a continuous release during the initial stages. After 60 days, the hydrated microspheres had not significantly degraded. Factors contributing to the lag time before significant release was observed include the high molecular weight (70k-100k) g/mol) and hydrophobic nature of PLGA resulting in slow hydration of the microspheres. Also, SEM analysis showed product spheres to be relatively free of defects reducing the possibility of a burst release.

Detailed Description Text (75):

In FIG. 10, lidocaine hydrochloride-PLGA formulations prepared by solvent extraction essentially dumped 70-90% of their core load in the first 24 hours with complete release within days. The increased surface area of these smaller diameter microspheres and their high surface porosity observed by SEM contribute to the observed release, as well as the high aqueous solubility of the incipient lidocaine hydrochloride. It appears that lidocaine hydrochloride is mostly surface-bound in the microsphere formulations rather than homogeneously distributed throughout the polymer matrix.

Detailed Description Text (76):

Sustained release formulations releasing the. anesthetic lidocaine have been prepared by o/w solvent.evaporation techniques resulting in continuous release for 7-10 days following a one week, burst-free lag time. Conversely, lidocaine hydrochloride-PLGA formulations prepared by w/o solvent extraction completely emptied their contents within the first few days.

Other Reference Publication (1):

Gilding, Biodegradable polymers for use in surgery-polyglycolic/poly (ac c acid) homo-and copolymers: 1, Polymer, vol. 20, Dec. 1979, pp1459-1464.

Other Reference Publication (6):

Jeyanthi, et al., Novel, Burst Free Programmable Biodegradable Microspheres For Controlled Release of Polypeptides, Proceedings Int. Symp. control Release Bioact. Mater. (1996) p351-352.

Other Reference Publication (7):

Yeh, A novel emulsification-solvent extraction technique for production of protein loaded biodegradable microparticles for vaccine and drug delivery, Journal of Controlled Release, 33 (1995) 437-445.

Other Reference Publication (8):

Yan, Characterization and morphological analysis of protein-loaded poly(lactide-co-glycolide) microparticles prepared by water-in-oil-in-water emulsion technique, Journal of Controlled Release, 32 (1994) 231-241.

Other Reference Publication (9):

Wang, et al., Influence of formulation methods on the in vitro controlled release of protein from poly (ester) microspheres Journal of Controlled Release, 17 (1991) 23-32.

Other Reference Publication (11):

THIS PAGE BLANK (USPTO)

Setterstrom, Controlled Release of Antibiotics From biodegradable Microcapsules For Wound infection Control, Chemical Abstracts, 1983, pp215-226.

Other Reference Publication (15):

McConnel, et al., Antigenic homology within human enterotoxigenic Escherichia coli fimbrial colonization factor antigens: CFA/I, coli-surface-associated antigens (CS) 1, CS2, CS4 and CS17, FEMS Microbiology Letters 61 (1989) 105-108.

CLAIMS:

1. A process for preparing controlled release microcapsule formulations characterized by burst-free, sustained, programmable release of non-steroidal, antiinflammatory drugs comprising: dissolving a non-steroidal, antiinflammatory drug and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a volatile organic solvent, dispersing the dissolved mixture in an aqueous phase containing an emulsion stabilizer, and evaporating the organic solvent phase to obtain non-steroidal antiinflammatory drug-loaded microspheres.

2. A process for preparing controlled release microcapsule formulations characterized by burst-free, sustained, programmable release of non-steroidal, antiinflammatory drugs comprising: dissolving a non-steroidal, antiinflammatory drug and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a polar organic solvent, dispersing the dissolved non-steroidal, antiinflammatory drug dissolved in a polar organic solvent in a non-polar organic phase, pouring the emulsion into a hydrocarbon solvent, extracting the polar organic phase into the hydrocarbon solvent to form microspheres.

3. A process of preparing a controlled release microcapsule formulation characterized by burst-free sustained programmable release of a long-acting local anesthetic comprising: dissolving the long-acting local anesthetic and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a volatile organic solvent, dispersing the long-acting local anesthetic and volatile organic solvent in an aqueous phase containing an emulsion stabilizer, and evaporating the volatile organic solvent to precipitate microspheres of long-lasting local anesthetic and poly(lactide/glycolide) microspheres.

4. The process of claim 1, wherein the biodegradable poly(lactide/glycolide) polymers comprise a ratio of lactide to glycolide from 100/0 to 50/50.

12. The process of claim 2, wherein the biodegradable poly(lactide/glycolide) polymers comprise a ratio of lactide to glycolide from 100/0 to 50/50.

THIS PAGE BLANK (USPTO)